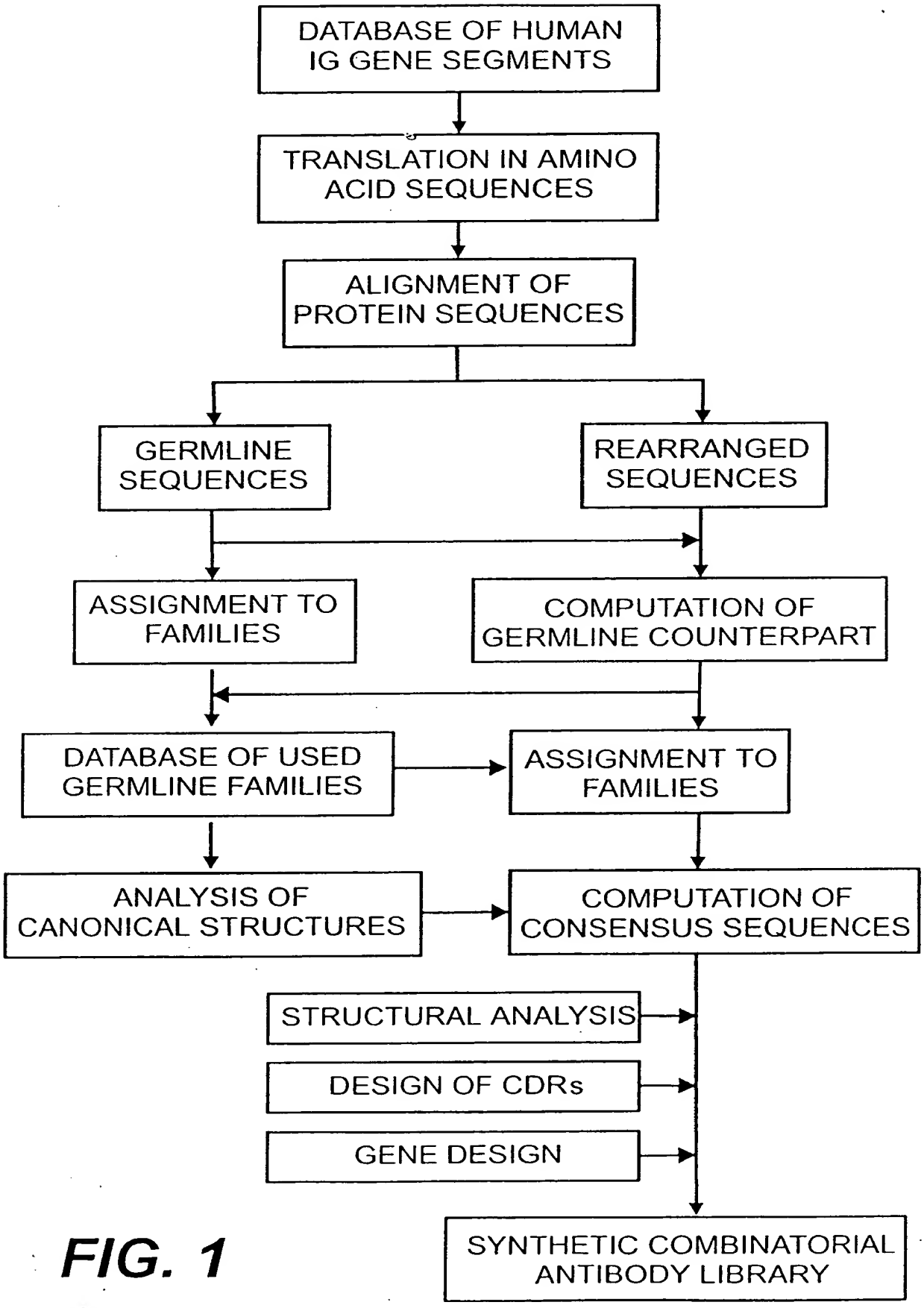

DATABASE OF HUMAN IG GENE SEGMENTS
TRANSLATION IN AMINO ACID SEQUENCES
ALIGNMENT OF PROTEIN SEQUENCES
GERMLINE SEQUENCES
REARRANGED SEQUENCES
ASSIGNMENT TO FAMILIES
COMPUTATION OF GERMLINE COUNTERPART
DATABASE OF USED GERMLINE FAMILIES
ASSIGNMENT TO FAMILIES
ANALYSIS OF CANONICAL STRUCTURES
COMPUTATION OF CONSENSUS SEQUENCES
STRUCTURAL ANALYSIS
DESIGN OF CDRs
GENE DESIGN
SYNTHETIC COMBINATORIAL ANTIBODY LIBRARY

FIG. 1

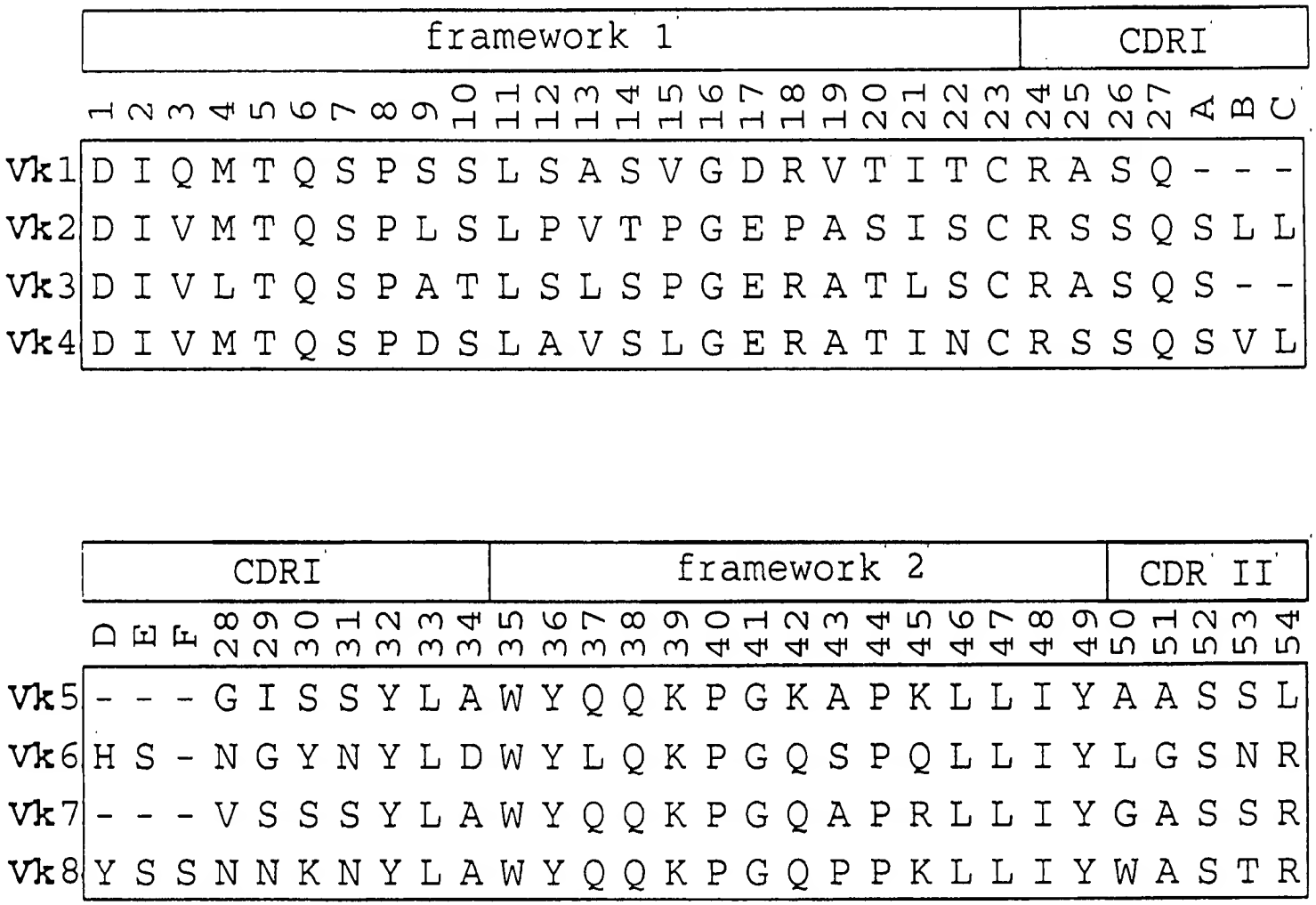

framework 1
CDRI
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 A B C
Vk1 D I Q M T Q S P S S L S A S V G D R V T I T C R A S Q - - -
Vk2 D I V M T Q S P L S L P V T P G E P A S I S C R S S Q S L L
Vk3 D I V L T Q S P A T L S L S P G E R A T L S C R A S Q S - -
Vk4 D I V M T Q S P D S L A V S L G E R A T I N C R S S Q S V L
CDRI
framework 2
CDR II
D E F 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54
Vk5 - - - G I S S Y L A W Y Q Q K P G K A P K L L I Y A A S S L
Vk6 H S - N G Y N Y L D W Y L Q K P G Q S P Q L L I Y L G S N R
Vk7 - - - V S S S Y L A W Y Q Q K P G Q A P R L L I Y G A S S R
Vk8 Y S S N N K N Y L A W Y Q Q K P G Q P P K L L I Y W A S T R

FIG. 2A

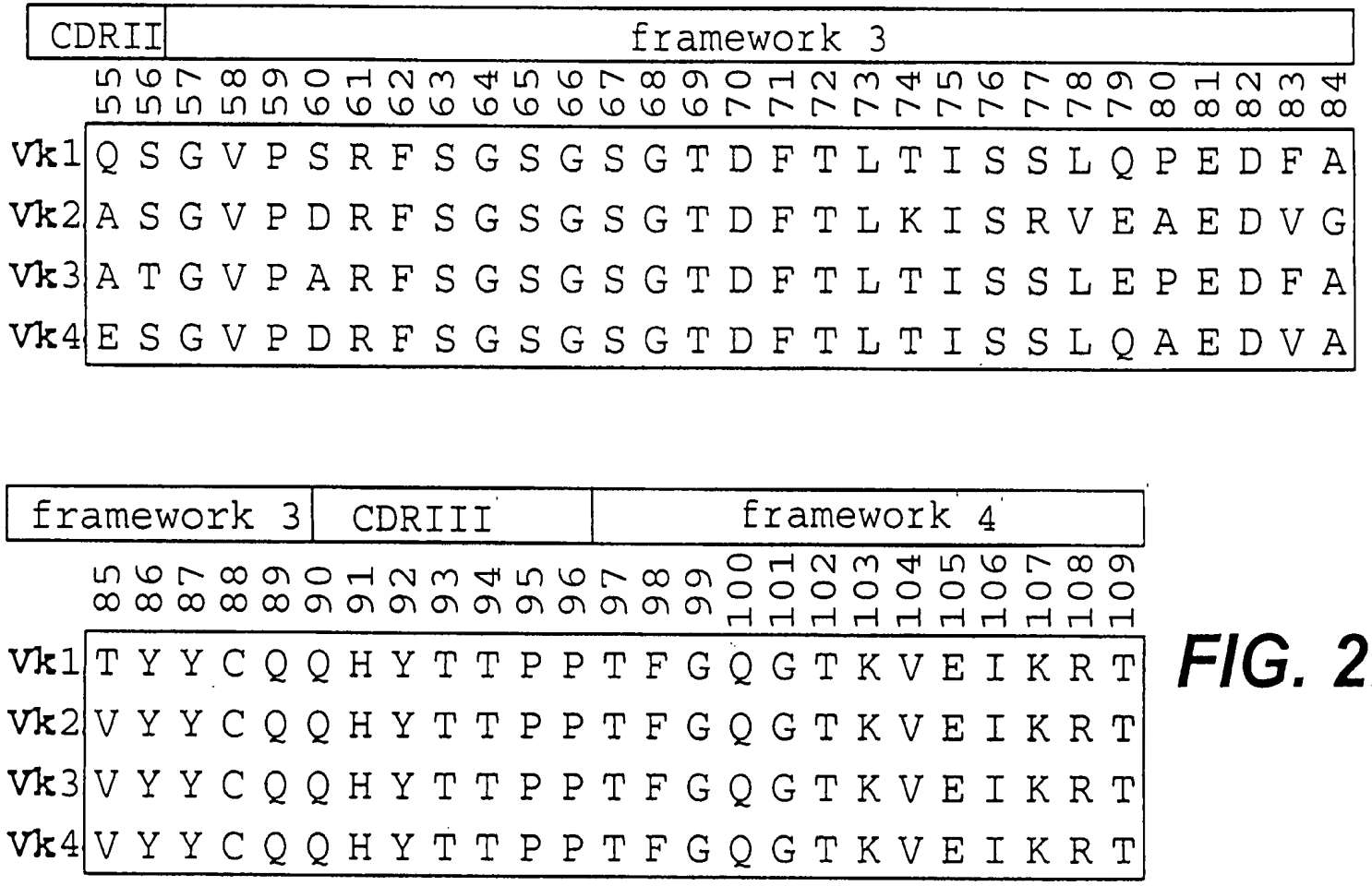

CDRII
framework 3
55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84
Vk1 Q S G V P S R F S G S G S G T D F T L T I S S L Q P E D F A
Vk2 A S G V P D R F S G S G S G T D F T L K I S R V E A E D V G
Vk3 A T G V P A R F S G S G S G T D F T L T I S S L E P E D F A
Vk4 E S G V P D R F S G S G S G T D F T L T I S S L Q A E D V A
framework 3
CDRIII
framework 4
85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109
Vk1 T Y Y C Q Q H Y T T P P T F G Q G T K V E I K R T
Vk2 V Y Y C Q Q H Y T T P P T F G Q G T K V E I K R T
Vk3 V Y Y C Q Q H Y T T P P T F G Q G T K V E I K R T
Vk4 V Y Y C Q Q H Y T T P P T F G Q G T K V E I K R T

FIG. 2B

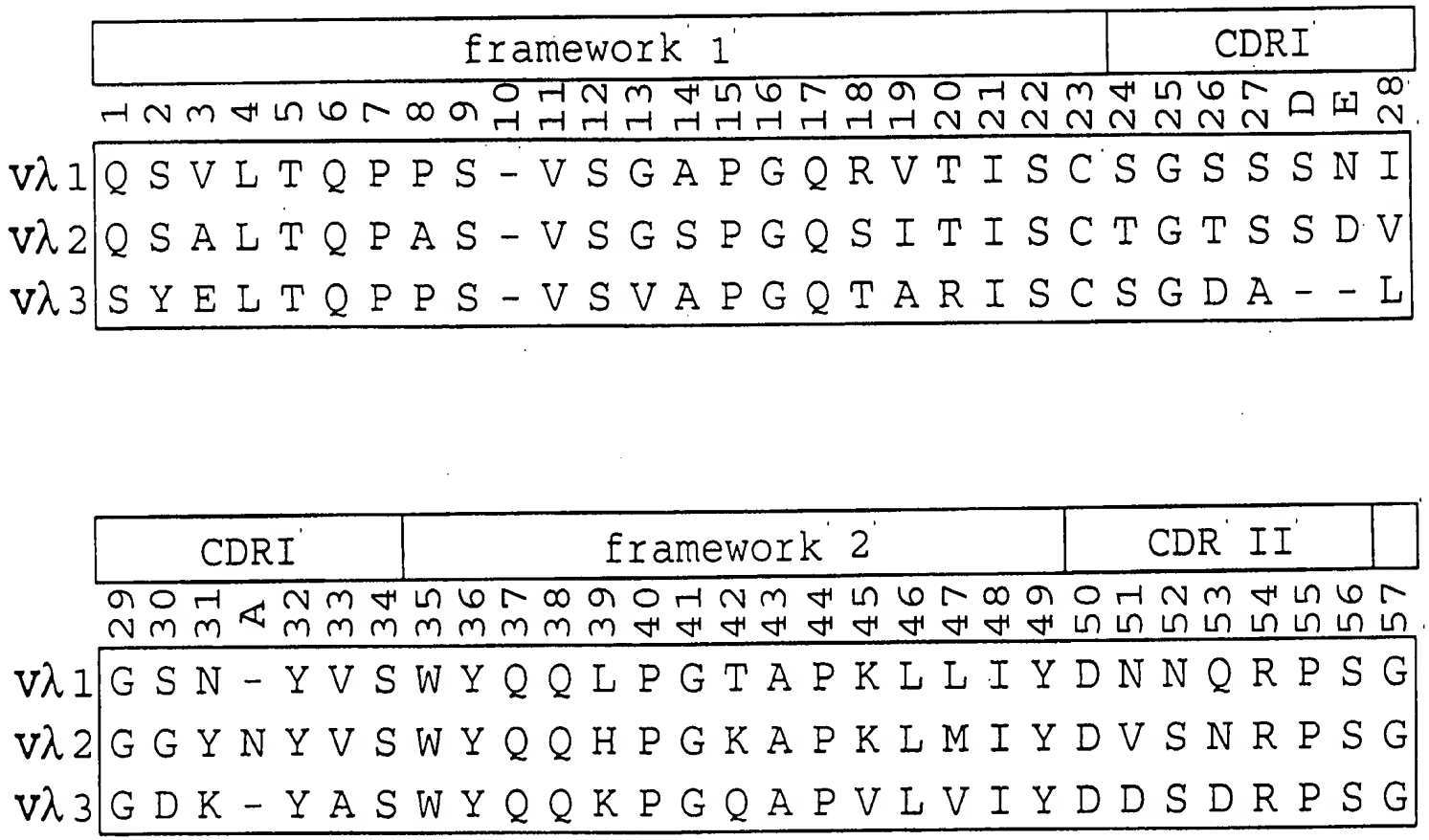

framework 1
CDRI
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 D E 28
vλ1 Q S V L T Q P P S - V S G A P G Q R V T I S C S G S S S N I
vλ2 Q S A L T Q P A S - V S G S P G Q S I T I S C T G T S S D V
vλ3 S Y E L T Q P P S - V S V A P G Q T A R I S C S G D A - - L
CDRI
framework 2
CDR II
29 30 31 A 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57
vλ1 G S N - Y V S W Y Q Q L P G T A P K L L I Y D N N Q R P S G
vλ2 G G Y N Y V S W Y Q Q H P G K A P K L M I Y D V S N R P S G
vλ3 G D K - Y A S W Y Q Q K P G Q A P V L V I Y D D S D R P S G

FIG. 2C

	framework 3																									
	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87
Vλ1	V	P	D	R	F	S	G	S	K	S	G	T	S	A	S	L	A	I	T	G	L	Q	S	E	D	E	A	D	Y	Y
Vλ2	V	S	N	R	F	S	G	S	K	S	G	N	T	A	S	L	T	I	S	G	L	Q	A	E	D	E	A	D	Y	Y
Vλ3	I	P	E	R	F	S	G	S	N	S	G	N	T	A	T	L	T	I	S	G	T	Q	A	E	D	E	A	D	Y	Y

		CDRIII								framework 4																
	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	A	107					
Vλ1	C	Q	Q	H	Y	T	T	P	P	V	F	G	G	G	T	K	L	T	V	L	G					
Vλ2	C	Q	Q	H	Y	T	T	P	P	V	F	G	G	G	T	K	L	T	V	L	G					
Vλ3	C	Q	Q	H	Y	T	T	P	P	V	F	G	G	G	T	K	L	T	V	L	G					

FIG. 2D

	framework 1																												
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
VH1A	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	S	S	V	K	V	S	C	K	A	S	G	G	T	F	S
VH1B	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S	V	K	V	S	C	K	A	S	G	Y	T	F	T
VH2	Q	V	Q	L	K	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	L	T	C	T	F	S	G	F	S	L	S
VH3	E	V	Q	L	V	E	S	G	G	G	L	V	Q	P	G	G	S	L	R	L	S	C	A	A	S	G	F	T	F	S
VH4	Q	V	Q	L	Q	E	S	G	P	G	L	V	K	P	S	E	T	L	S	L	T	C	T	V	S	G	G	S	I	S
VH5	E	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	E	S	L	K	I	S	C	K	G	S	G	Y	S	F	T
VH6	Q	V	Q	L	Q	Q	S	G	P	G	L	V	K	P	S	Q	T	L	S	L	T	C	A	I	S	G	D	S	V	S

	CDRI								framework 2														CDR II							
	31	A	B	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	A	B	C	53	54	55	56	57
VH1A	S	-	-	Y	A	I	S	W	V	R	Q	A	P	G	Q	G	L	E	W	M	G	G	I	I	P	-	-	I	F	G	T	A
VH1B	S	-	-	Y	Y	M	H	W	V	R	Q	A	P	G	Q	G	L	E	W	M	G	W	I	N	P	-	-	N	S	G	G	T
VH2	T	S	G	V	G	V	G	W	I	R	Q	P	P	G	K	A	L	E	W	L	A	L	I	D	-	-	-	W	D	D	D	K
VH3	S	-	-	Y	A	M	S	W	V	R	Q	A	P	G	K	G	L	E	W	V	S	A	I	S	G	-	-	S	G	G	S	T
VH4	S	-	-	Y	Y	W	S	W	I	R	Q	P	P	G	K	G	L	E	W	I	G	Y	I	Y	-	-	-	Y	S	G	S	T
VH5	S	-	-	Y	W	I	G	W	V	R	Q	M	P	G	K	G	L	E	W	M	G	I	I	Y	P	-	-	G	D	S	D	T

FIG. 2E

VH6	S	N	S	A	A	W	N	W	I	R	Q	S	P	G	R	G	L	E	W	L	G	R	T	Y	Y	R	-	S	K	W	Y	N

	CDRII										framework 3																				
	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	A	B	C	83	84	85
VH1A	N	Y	A	Q	K	F	Q	G	R	V	T	I	T	A	D	E	S	T	S	T	A	Y	M	E	L	S	S	L	R	S	E
VH1B	N	Y	A	Q	K	F	Q	G	R	V	T	M	T	R	D	T	S	I	S	T	A	Y	M	E	L	S	S	L	R	S	E
VH2	Y	Y	S	T	S	L	K	T	R	L	T	I	S	K	D	T	S	K	N	Q	V	V	L	T	M	T	N	M	D	P	V
VH3	Y	Y	A	D	S	V	K	G	R	F	T	I	S	R	D	N	S	K	N	T	L	Y	L	Q	M	N	S	L	R	A	E
VH4	N	Y	N	P	S	L	K	S	R	V	T	I	S	V	D	T	S	K	N	Q	F	S	L	K	L	S	S	V	T	A	A
VH5	R	Y	S	P	S	F	Q	G	Q	V	T	I	S	A	D	K	S	I	S	T	A	Y	L	Q	W	S	S	L	K	A	S
VH6	D	Y	A	V	S	V	K	S	R	I	T	I	N	P	D	T	S	K	N	Q	F	S	L	Q	L	N	S	V	T	P	E

	framework 3										CDRII													framework 4							
	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	A	B	C	101	102	103	104	105	106	107	108	109	110	111	112	113
VH1A	D	T	A	V	Y	Y	C	A	R	W	G	G	D	G	F	Y	A	M	D	Y	W	G	Q	G	T	L	V	T	V	S	S
VH1B	D	T	A	V	Y	Y	C	A	R	W	G	G	D	G	F	Y	A	M	D	Y	W	G	Q	G	T	L	V	T	V	S	S
VH2	D	T	A	T	Y	Y	C	A	R	W	G	G	D	G	F	Y	A	M	D	Y	W	G	Q	G	T	L	V	T	V	S	S
VH3	D	T	A	V	Y	Y	C	A	R	W	G	G	D	G	F	Y	A	M	D	Y	W	G	Q	G	T	L	V	T	V	S	S
VH4	D	T	A	V	Y	Y	C	A	R	W	G	G	D	G	F	Y	A	M	D	Y	W	G	Q	G	T	L	V	T	V	S	S

FIG. 2F

VH5	D T A M Y Y C A R W G G D G F Y A M D Y W G Q G T L V T V S S
VH6	D T A V Y Y C A R W G G D G F Y A M D Y W G Q G T L V T V S S

FIG. 2G

```
.D  I  Q  M   T  Q  S   P  S  S   L  S  A  S   V  G  D
 EcoRV            BanII
~~~~~~           ~~~~~~~~
GATATCCAGA TGACCCAGAG CCCGTCTAGC CTGAGCGCGA GCGTGGGTGA
CTATAGGTCT ACTGGGTCTC GGGCAGATCG GACTCGCGCT CGCACCCACT

  R  V  T   I  T  C  R   A  S  Q   G  I  S   S  Y  L
                PstI
               ~~~~~~~~
TCGTGTGACC ATTACCTGCA GAGCGAGCCA GGGCATTAGC AGCTATCTGG
AGCACACTGG TAATGGACGT CTCGCTCGGT CCCGTAATCG TCGATAGACC

A  W  Y  Q   Q  K  P  G  K  A  P   K  L  L   I  Y  A
   KpnI          SexAI                AseI
  ~~~~~~        ~~~~~~~~             ~~~~~~~
CGTGGTACCA GCAGAAACCA GGTAAAGCAC CGAAACTATT AATTTATGCA
GCACCATGGT CGTCTTTGGT CCATTTCGTG GCTTTGATAA TTAAATACGT

 A  S  S  L   Q  S  G   V  P  S   R  F  S  G   S  G  S
                  SanDI                        BamHI
               ~~~~~~~~                       ~~~~~
GCCAGCAGCT TGCAAAGCGG GGTCCCGTCC CGTTTTAGCG GCTCTGGATC
CGGTCGTCGA ACGTTTCGCC CCAGGGCAGG GCAAAATCGC CGAGACCTAG
```

FIG. 3A

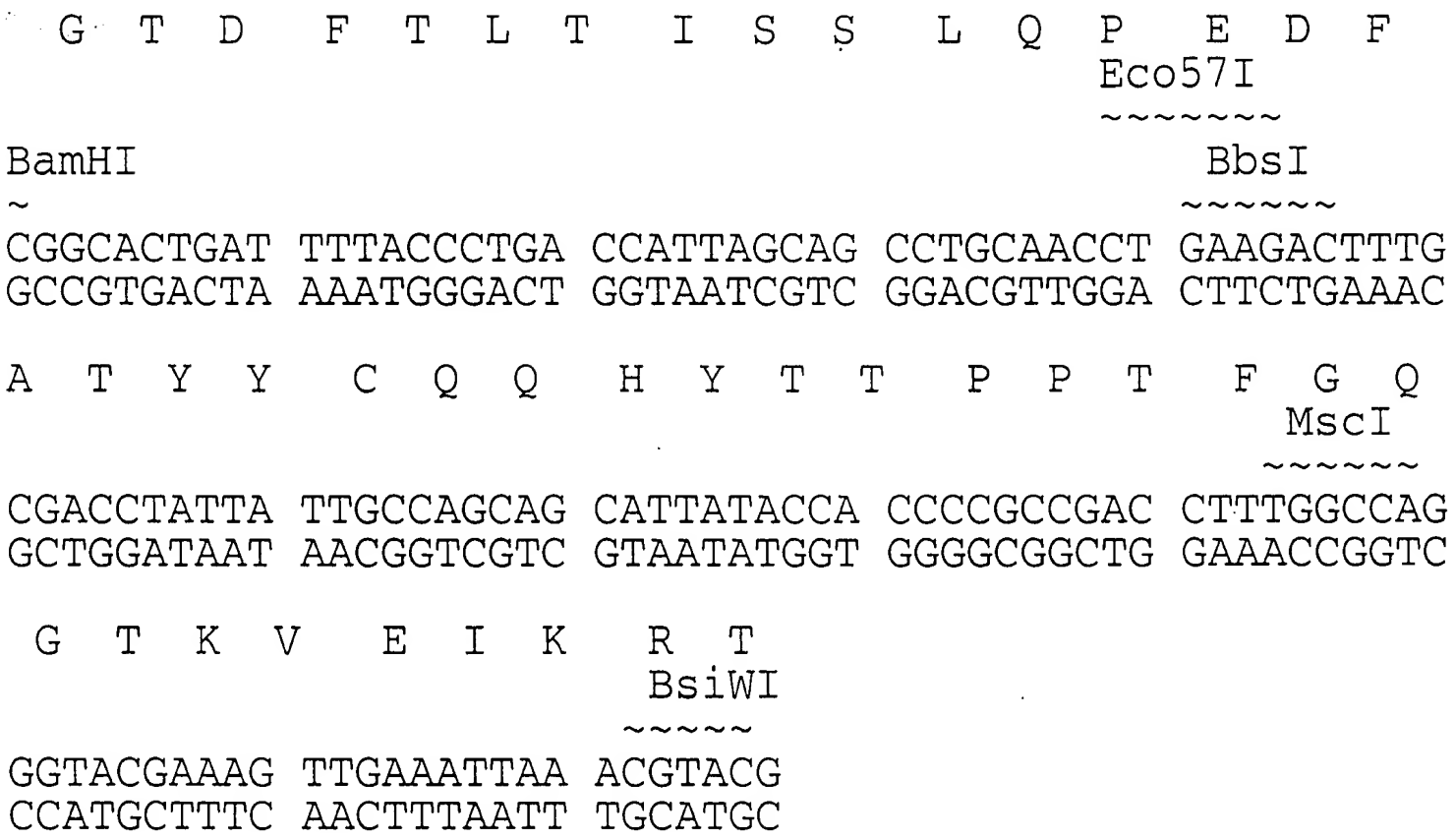

G T D F T L T I S S L Q P E D F
Eco57I
BamHI
BbsI
CGGCACTGAT TTTACCCTGA CCATTAGCAG CCTGCAACCT GAAGACTTTG
GCCGTGACTA AAATGGGACT GGTAATCGTC GGACGTTGGA CTTCTGAAAC
A T Y Y C Q Q H Y T T P P T F G Q
MscI
CGACCTATTA TTGCCAGCAG CATTATACCA CCCCGCCGAC CTTTGGCCAG
GCTGGATAAT AACGGTCGTC GTAATATGGT GGGGCGGCTG GAAACCGGTC
G T K V E I K R T
BsiWI
GGTACGAAAG TTGAAATTAA ACGTACG
CCATGCTTTC AACTTTAATT TGCATGC

FIG. 3B

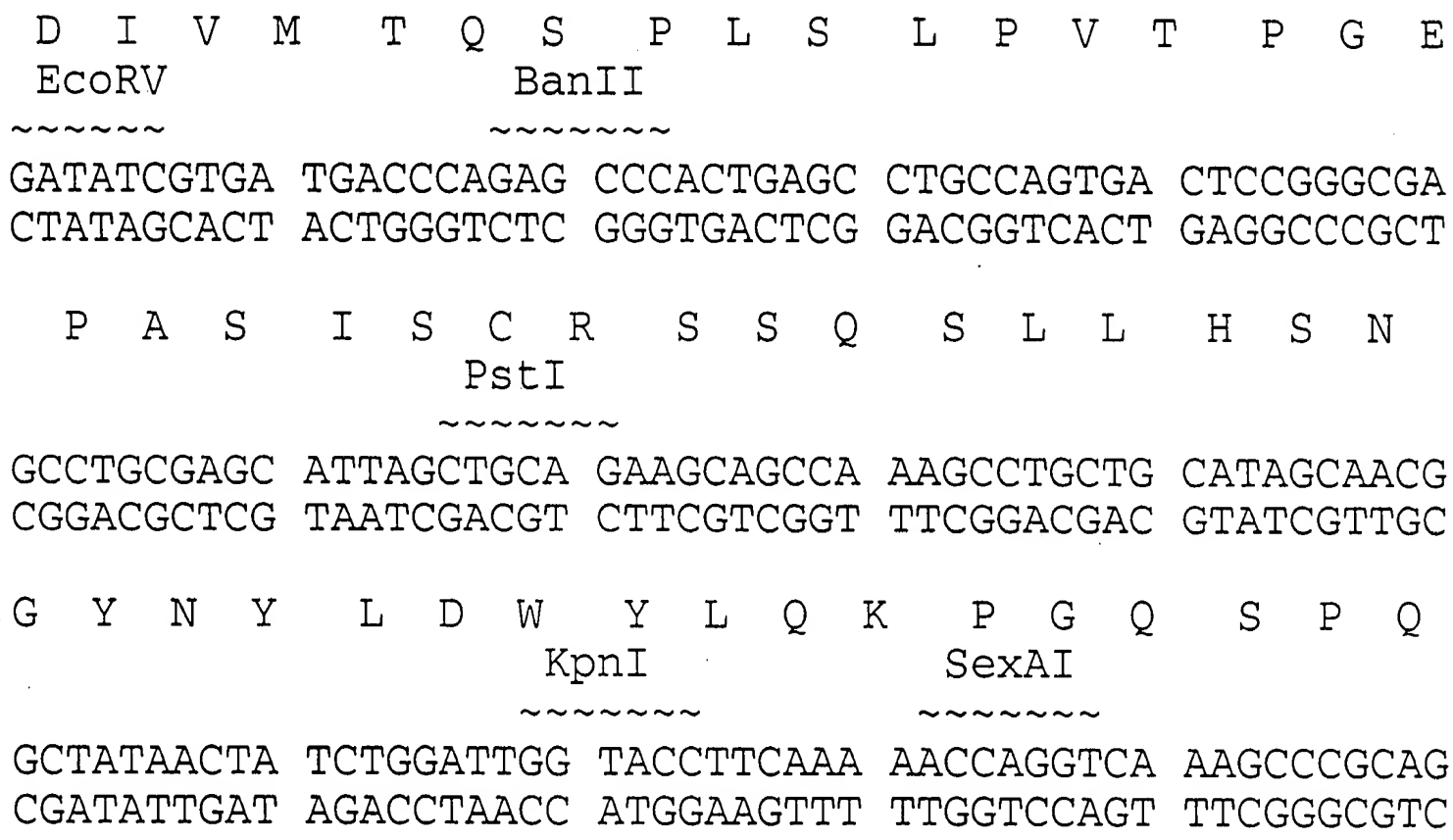

D I V M T Q S P L S L P V T P G E
EcoRV
BanII
GATATCGTGA TGACCCAGAG CCCACTGAGC CTGCCAGTGA CTCCGGGCGA
CTATAGCACT ACTGGGTCTC GGGTGACTCG GACGGTCACT GAGGCCCGCT
P A S I S C R S S Q S L L H S N
PstI
GCCTGCGAGC ATTAGCTGCA GAAGCAGCCA AAGCCTGCTG CATAGCAACG
CGGACGCTCG TAATCGACGT CTTCGTCGGT TTCGGACGAC GTATCGTTGC
G Y N Y L D W Y L Q K P G Q S P Q
KpnI
SexAI
GCTATAACTA TCTGGATTGG TACCTTCAAA AACCAGGTCA AAGCCCGCAG
CGATATTGAT AGACCTAACC ATGGAAGTTT TTGGTCCAGT TTCGGGCGTC

FIG. 3C

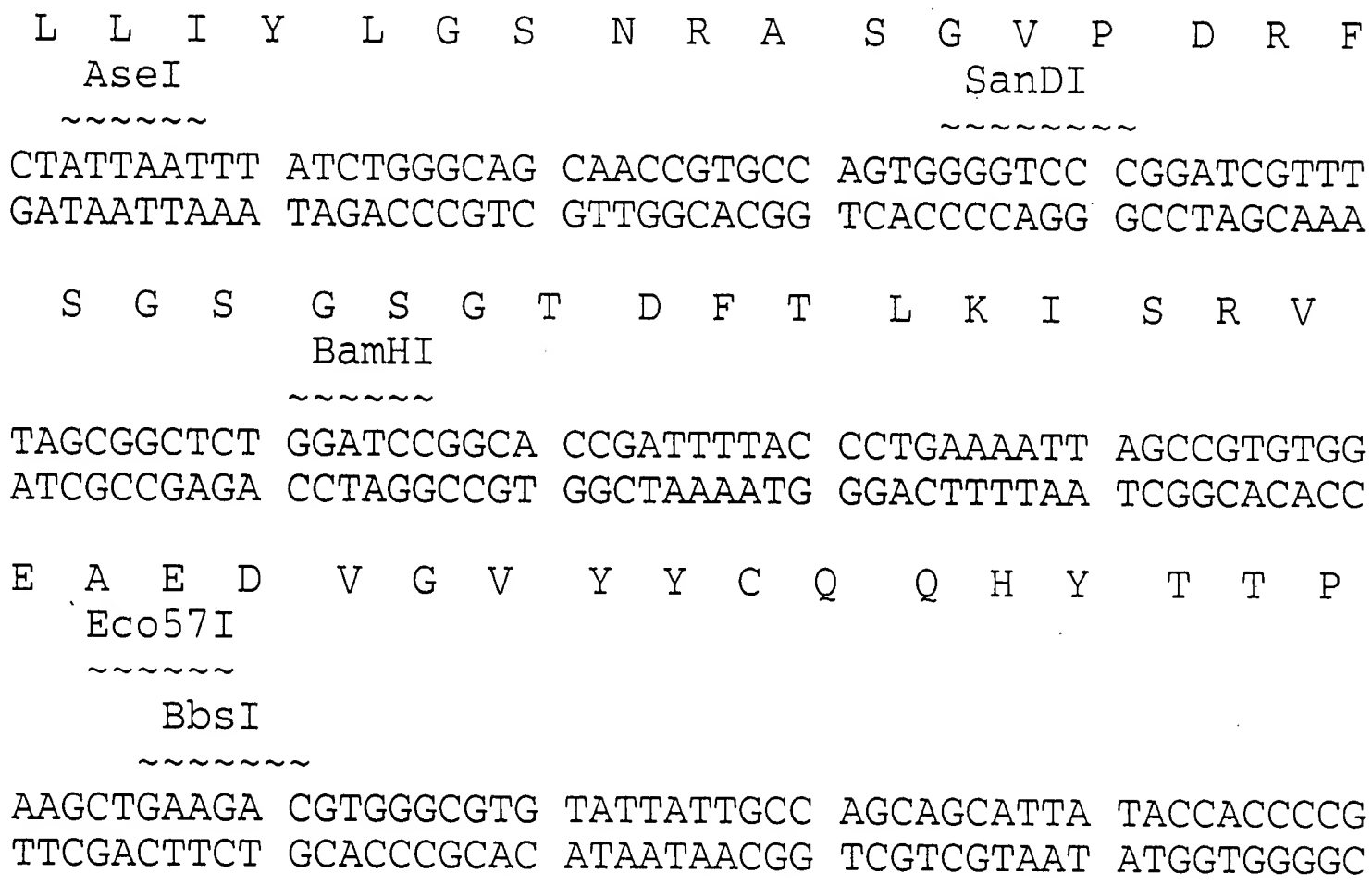

L L I Y L G S N R A S G V P D R F
AseI
SanDI
CTATTAATTT ATCTGGGCAG CAACCGTGCC AGTGGGGTCC CGGATCGTTT
GATAATTAAA TAGACCCGTC GTTGGCACGG TCACCCCAGG GCCTAGCAAA
S G S G S G T D F T L K I S R V
BamHI
TAGCGGCTCT GGATCCGGCA CCGATTTTAC CCTGAAAATT AGCCGTGTGG
ATCGCCGAGA CCTAGGCCGT GGCTAAAATG GGACTTTTAA TCGGCACACC
E A E D V G V Y Y C Q Q H Y T T P
Eco57I
BbsI
AAGCTGAAGA CGTGGGCGTG TATTATTGCC AGCAGCATTA TACCACCCCG
TTCGACTTCT GCACCCGCAC ATAATAACGG TCGTCGTAAT ATGGTGGGGC

FIG. 3D

```
P   T   F   G   Q   G   T   K   V   E   I   K   R   T
        MscI                                    BsiWI
      ~~~~~~~~                                ~~~~~~~
CCGACCTTTG GCCAGGGTAC GAAAGTTGAA ATTAAACGTA CG
GGCTGGAAAC CGGTCCCATG CTTTCAACTT TAATTTGCAT GC
```

FIG. 3E


D I V L T Q S P A T L S L S P G E
EcoRV
BanII
GATATCGTGC TGACCCAGAG CCCGGCGACC CTGAGCCTGT CTCCGGGCGA
CTATAGCACG ACTGGGTCTC GGGCCGCTGG GACTCGGACA GAGGCCCGCT
R A T L S C R A S Q S V S S S Y
PstI
ACGTGCGACC CTGAGCTGCA GAGCGAGCCA GAGCGTGAGC AGCAGCTATC
TGCACGCTGG GACTCGACGT CTCGCTCGGT CTCGCACTCG TCGTCGATAG
L A W Y Q Q K P G Q A P R L L I Y
KpnI
SexAI
AseI

FIG. 3F

```
TGGCGTGGTA CCAGCAGAAA CCAGGTCAAG CACCGCGTCT ATTAATTTAT
ACCGCACCAT GGTCGTCTTT GGTCCAGTTC GTGGCGCAGA TAATTAAATA

 G  A  S  S  R  A  T  G  V  P  A  R  F  S  G  S  G
                      SanDI                  BamHI
                      ~~~~~~~                  ~~
GGCGCGAGCA GCCGTGCAAC TGGGGTCCCG GCGCGTTTTA GCGGCTCTGG
CCGCGCTCGT CGGCACGTTG ACCCCAGGGC CGCGCAAAAT CGCCGAGACC

  S  G  T  D  F  T  L  T  I  S  S  L  E  P  E  D
                                        Eco57I
                                        ~~~~~~
BamHI                                     BbsI
~~~~                                      ~~~~~~
ATCCGGCACG GATTTTACCC TGACCATTAG CAGCCTGGAA CCTGAAGACT
TAGGCCGTGC CTAAAATGGG ACTGGTAATC GTCGGACCTT GGACTTCTGA
```

FIG. 3G

```
F  A  V  Y   Y  C  Q   Q  H  Y  T   T  P  P   T  F  G
                                                MscI
                                                ~~~~
TTGCGGTGTA TTATTGCCAG CAGCATTATA CCACCCCGCC GACCTTTGGC
AACGCCACAT AATAACGGTC GTCGTAATAT GGTGGGGCGG CTGGAAACCG

 Q  G  T  K   V  E  I   K  R  T
MscI                    BsiWI
~~                      ~~~~~~
CAGGGTACGA AAGTTGAAAT TAAACGTACG
GTCCCATGCT TTCAACTTTA ATTTGCATGC
```

FIG. 3H

```
 D  I  V  M     T  Q  S     P  D  S     L  A  V  S     L  G  E
 EcoRV                BanII
~~~~~~              ~~~~~~~
GATATCGTGA TGACCCAGAG CCCGGATAGC CTGGCGGTGA GCCTGGGCGA
CTATAGCACT ACTGGGTCTC GGGCCTATCG GACCGCCACT CGGACCCGCT

  R  A  T     I  N  C  R     S  S  Q     S  V  L     Y  S  S
                  PstI
                ~~~~~~~
ACGTGCGACC ATTAACTGCA GAAGCAGCCA GAGCGTGCTG TATAGCAGCA
TGCACGCTGG TAATTGACGT CTTCGTCGGT CTCGCACGAC ATATCGTCGT

N  N  K  N     Y  L  A     W  Y  Q  Q     K  P  G     Q  P  P
                           KpnI              SexAI
                         ~~~~~~            ~~~~~~~~
ACAACAAAAA CTATCTGGCG TGGTACCAGC AGAAACCAGG TCAGCCGCCG
TGTTGTTTTT GATAGACCGC ACCATGGTCG TCTTTGGTCC AGTCGGCGGC
```

FIG. 3I

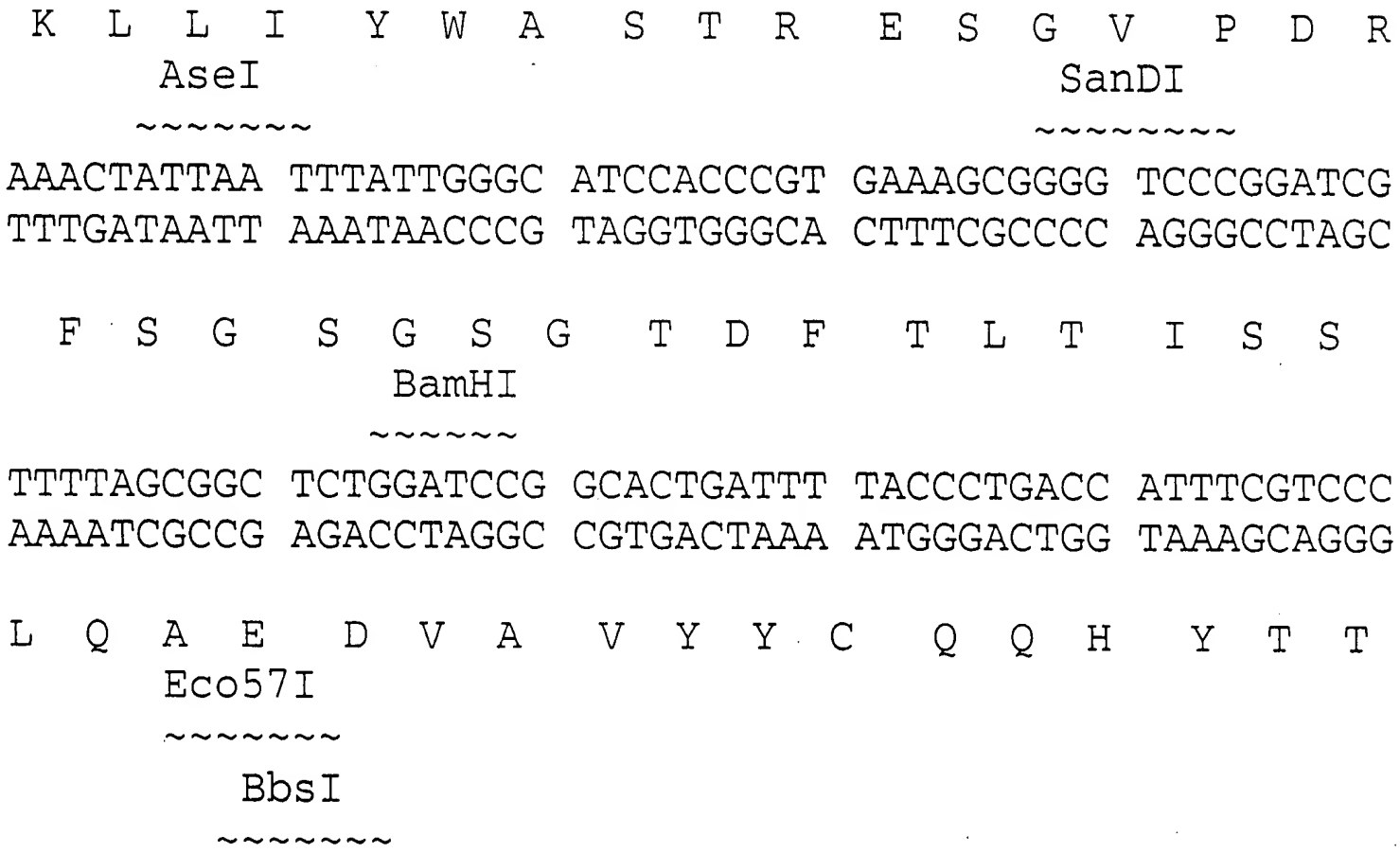

K L L I Y W A S T R E S G V P D R
AseI
SanDI
AAACTATTAA TTTATTGGGC ATCCACCCGT GAAAGCGGGG TCCCGGATCG
TTTGATAATT AAATAACCCG TAGGTGGGCA CTTTCGCCCC AGGGCCTAGC
F S G S G S G T D F T L T I S S
BamHI
TTTTAGCGGC TCTGGATCCG GCACTGATTT TACCCTGACC ATTTCGTCCC
AAAATCGCCG AGACCTAGGC CGTGACTAAA ATGGGACTGG TAAAGCAGGG
L Q A E D V A V Y Y C Q Q H Y T T
Eco57I
BbsI

FIG. 3J

```
TGCAAGCTGA AGACGTGGCG GTGTATTATT GCCAGCAGCA TTATACCACC
ACGTTCGACT TCTGCACCGC CACATAATAA CGGTCGTCGT AATATGGTGG

 P  P  T  F   G  Q  G   T  K  V   E  I  K  R   T
            MscI                              BsiWI
           ~~~~~~                            ~~~~~~
CCGCCGACCT TTGGCCAGGG TACGAAAGTT GAAATTAAAC GTACG
GGCGGCTGGA AACCGGTCCC ATGCTTTCAA CTTTAATTTG CATGC
```

FIG. 3K

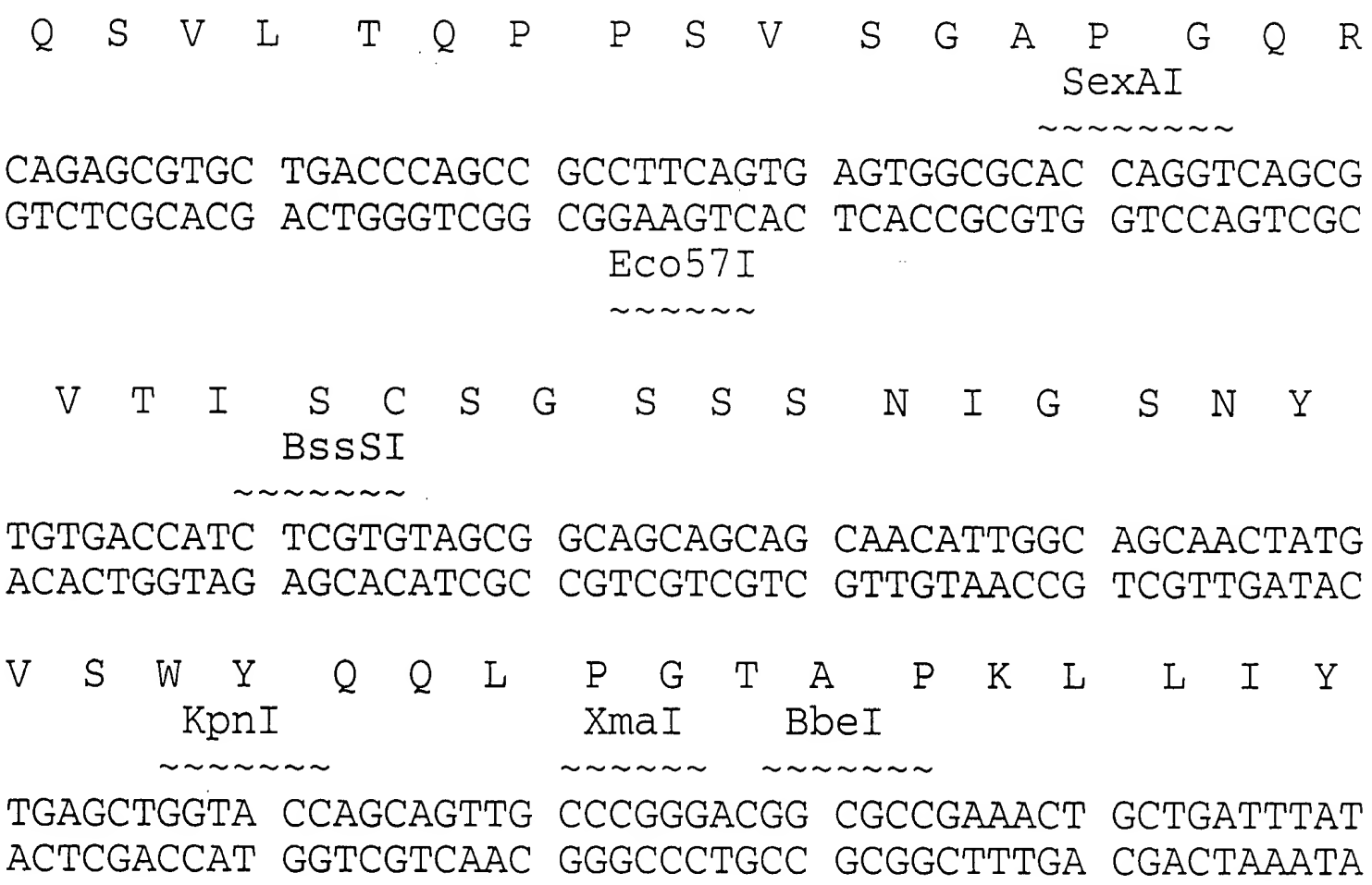

Q S V L T Q P P S V S G A P G Q R
SexAI
CAGAGCGTGC TGACCCAGCC GCCTTCAGTG AGTGGCGCAC CAGGTCAGCG
GTCTCGCACG ACTGGGTCGG CGGAAGTCAC TCACCGCGTG GTCCAGTCGC
Eco57I
V T I S C S G S S S N I G S N Y
BssSI
TGTGACCATC TCGTGTAGCG GCAGCAGCAG CAACATTGGC AGCAACTATG
ACACTGGTAG AGCACATCGC CGTCGTCGTC GTTGTAACCG TCGTTGATAC
V S W Y Q Q L P G T A P K L L I Y
KpnI
XmaI
BbeI
TGAGCTGGTA CCAGCAGTTG CCCGGGACGG CGCCGAAACT GCTGATTTAT
ACTCGACCAT GGTCGTCAAC GGGCCCTGCC GCGGCTTTGA CGACTAAATA

FIG. 4A

```
 D  N  N  Q   R  P  S   G  V  P   D  R  F  S   G  S  K
                Bsu36I                        BamHI
                ~~~~~~~~                      ~~~~~~
GATAACAACC AGCGTCCCTC AGGCGTGCCG GATCGTTTTA GCGGATCCAA
CTATTGTTGG TCGCAGGGAG TCCGCACGGC CTAGCAAAAT CGCCTAGGTT

  S  G  T   S  A  S  L   A  I  T   G  L  Q   S  E  D
                                              BbsI
                                              ~~~~~~
AAGCGGCACC AGCGCGAGCC TTGCGATTAC GGGCCTGCAA AGCGAAGACG
TTCGCCGTGG TCGCGCTCGG AACGCTAATG CCCGGACGTT TCGCTTCTGC

E  A  D  Y   Y  C  Q   Q  H  Y  T   T  P  P   V  F  G
AAGCGGATTA TTATTGCCAG CAGCATTATA CCACCCCGCC TGTGTTTGGC
TTCGCCTAAT AATAACGGTC GTCGTAATAT GGTGGGGCGG ACACAAACCG
```

FIG. 4B

```
 G  G  T  K   L  T  V   L  G
            HpaI       MscI
           ~~~~~~      ~~~
GGCGGCACGA AGTTAACCGT TCTTGGC
CCGCCGTGCT TCAATTGGCA AGAACCG
```

FIG. 4C


Q S A L T Q P A S V S G S P G Q S
SexAI
CAGAGCGCAC TGACCCAGCC AGCTTCAGTG AGCGGCTCAC CAGGTCAGAG
GTCTCGCGTG ACTGGGTCGG TCGAAGTCAC TCGCCGAGTG GTCCAGTCTC
Eco57I
I T I S C T G T S S D V G G Y N
BssSI
CATTACCATC TCGTGTACGG GTACTAGCAG CGATGTGGGC GGCTATAACT
GTAATGGTAG AGCACATGCC CATGATCGTC GCTACACCCG CCGATATTGA
Y V S W Y Q Q H P G K A P K L M I
KpnI XmaI BbeI
ATGTGAGCTG GTACCAGCAG CATCCCGGGA AGGCGCCGAA ACTGATGATT
TACACTCGAC CATGGTCGTC GTAGGGCCCT TCCGCGGCTT TGACTACTAA

FIG. 4D

```
 Y  D  V  S   N  R  P   S  G  V   S  N  R  F   S  G  S
                    Bsu36I                      BamHI
                    ~~~~~~~~                    ~~~~~
TATGATGTGA GCAACCGTCC CTCAGGCGTG AGCAACCGTT TTAGCGGATC
ATACTACACT CGTTGGCAGG GAGTCCGCAC TCGTTGGCAA AATCGCCTAG

  K  S  G   N  T  A  S   L  T  I   S  G  L   Q  A  E
BamHI                                          BbsI
~                                              ~~~~
CAAAAGCGGC AACACCGCGA GCCTGACCAT TAGCGGCCTG CAAGCGGAAG
GTTTTCGCCG TTGTGGCGCT CGGACTGGTA ATCGCCGGAC GTTCGCCTTC

D  E  A  D   Y  Y  C   Q  Q  H  Y   T  T  P   P  V  F
BbsI
~~
ACGAAGCGGA TTATTATTGC CAGCAGCATT ATACCACCCC GCCTGTGTTT
TGCTTCGCCT AATAATAACG GTCGTCGTAA TATGGTGGGG CGGACACAAA
```

FIG. 4E

```
 G   G   G   T   K   L   T   V   L   G
                   HpaI        MscI
                  ~~~~~~      ~~~~
GGCGGCGGCA CGAAGTTAAC CGTTCTTGGC
CCGCCGCCGT GCTTCAATTG GCAAGAACCG
```

FIG. 4F

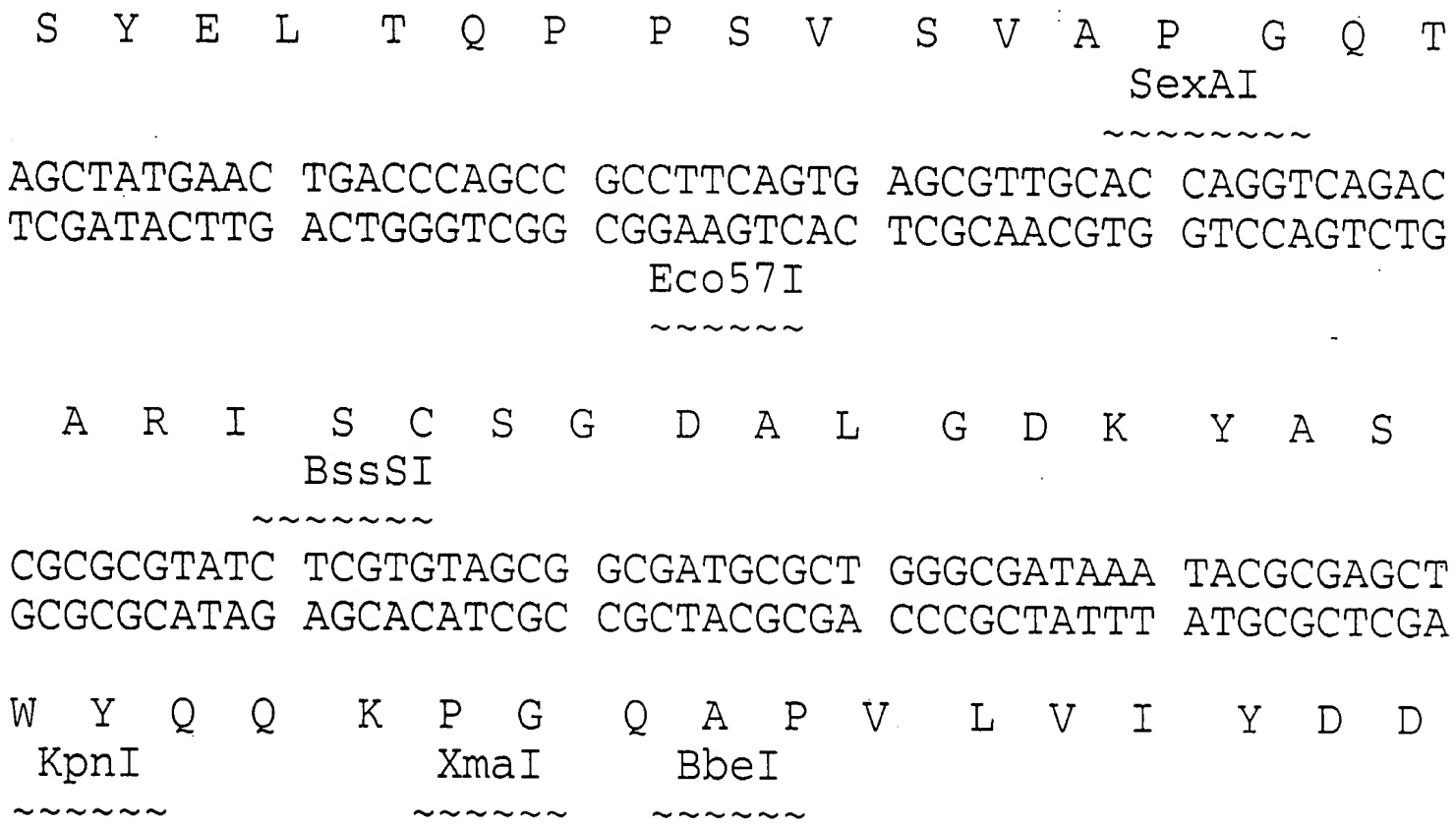

S Y E L T Q P P S V S V A P G Q T
SexAI
AGCTATGAAC TGACCCAGCC GCCTTCAGTG AGCGTTGCAC CAGGTCAGAC
TCGATACTTG ACTGGGTCGG CGGAAGTCAC TCGCAACGTG GTCCAGTCTG
Eco57I
A R I S C S G D A L G D K Y A S
BssSI
CGCGCGTATC TCGTGTAGCG GCGATGCGCT GGGCGATAAA TACGCGAGCT
GCGCGCATAG AGCACATCGC CGCTACGCGA CCCGCTATTT ATGCGCTCGA
W Y Q Q K P G Q A P V L V I Y D D
KpnI
XmaI
BbeI

FIG. 4G

```
GGTACCAGCA GAAACCCGGG CAGGCGCCAG TTCTGGTGAT TTATGATGAT
CCATGGTCGT CTTTGGGCCC GTCCGCGGTC AAGACCACTA AATACTACTA

 S  D  R  P  S  G  I  P  E  R  F  S  G  S  N  S  G
          Bsu36I                    BamHI
          ~~~~~~~                   ~~~~~~~
TCTGACCGTC CCTCAGGCAT CCCGGAACGC TTTAGCGGAT CCAACAGCGG
AGACTGGCAG GGAGTCCGTA GGGCCTTGCG AAATCGCCTA GGTTGTCGCC

 N  T  A  T  L  T  I  S  G  T  Q  A  E  D  E  A
                                   BbsI
                                   ~~~~~~~
```

FIG. 4H

```
CAACACCGCG ACCCTGACCA TTAGCGGCAC TCAGGCGGAA GACGAAGCGG
GTTGTGGCGC TGGGACTGGT AATCGCCGTG AGTCCGCCTT CTGCTTCGCC

D  Y  Y  C   Q  Q  H   Y  T  T  P   P  V  F   G  G  G
ATTATTATTG CCAGCAGCAT TATACCACCC CGCCTGTGTT TGGCGGCGGC
TAATAATAAC GGTCGTCGTA ATATGGTGGG GCGGACACAA ACCGCCGCCG

 T  K  L  T   V  L  G
     HpaI        MscI
    ~~~~~~~     ~~~~
ACGAAGTTAA CCGTTCTTGG C
TGCTTCAATT GGCAAGAACC G
```

FIG. 4I

```
 Q  V  Q  L   V  Q  S   G  A  E   V  K  K  P   G  S  S
       MfeI
      ~~~~~~~
CAGGTGCAAT TGGTTCAGTC TGGCGCGGAA GTGAAAAAAC CGGGCAGCAG
GTCCACGTTA ACCAAGTCAG ACCGCGCCTT CACTTTTTTG GCCCGTCGTC

  V  K  V   S  C  K  A   S  G  G   T  F  S   S  Y  A
                        BspEI
                       ~~~~~~
CGTGAAAGTG AGCTGCAAAG CCTCCGGAGG CACTTTTAGC AGCTATGCGA
GCACTTTCAC TCGACGTTTC GGAGGCCTCC GTGAAAATCG TCGATACGCT

I  S  W  V   R  Q  A   P  G  Q  G   L  E  W   M  G  G
               BstXI                 XhoI
            ~~~~~~~~~~~~~         ~~~~~~
TTAGCTGGGT GCGCCAAGCC CCTGGGCAGG GTCTCGAGTG GATGGGCGGC
AATCGACCCA CGCGGTTCGG GGACCCGTCC CAGAGCTCAC CTACCCGCCG
```

FIG. 5A

```
 I  I  P  I   F  G  T   A  N  Y   A  Q  K  F   Q  G  R
ATTATTCCGA TTTTTGGCAC GGCGAACTAC GCGCAGAAGT TTCAGGGCCG
TAATAAGGCT AAAAACCGTG CCGCTTGATG CGCGTCTTCA AAGTCCCGGC

  V  T  I   T  A  D  E   S  T  S   T  A  Y   M  E  L
BstEII
~~~~~~~
GGTGACCATT ACCGCGGATG AAAGCACCAG CACCGCGTAT ATGGAACTGA
CCACTGGTAA TGGCGCCTAC TTTCGTGGTC GTGGCGCATA TACCTTGACT

S  S  L  R   S  E  D   T  A  V  Y   Y  C  A   R  W  G
                       EagI          BssHII
                       ~~~~~~        ~~~~~~~
GCAGCCTGCG TAGCGAAGAT ACGGCCGTGT ATTATTGCGC GCGTTGGGGC
CGTCGGACGC ATCGCTTCTA TGCCGGCACA TAATAACGCG CGCAACCCCG
```

FIG. 5B

```
 G  D  G  F   Y  A  M   D  Y  W   G  Q  G  T   L  V  T
                                    StyI
                                   ~~~~~~
GGCGATGGCT TTTATGCGAT GGATTATTGG GGCCAAGGCA CCCTGGTGAC
CCGCTACCGA AAATACGCTA CCTAATAACC CCGGTTCCGT GGGACCACTG

  V  S  S
     BlpI
    ~~~~~~
GGTTAGCTCA G
CCAATCGAGT C
```

FIG. 5C


Q V Q L V Q S G A E V K K P G A S
MfeI
CAGGTGCAAT TGGTTCAGAG CGGCGCGGAA GTGAAAAAAC CGGGCGCGAG
GTCCACGTTA ACCAAGTCTC GCCGCGCCTT CACTTTTTTG GCCCGCGCTC
V K V S C K A S G Y T F T S Y Y
BspEI
CGTGAAAGTG AGCTGCAAAG CCTCCGGATA TACCTTTACC AGCTATTATA
GCACTTTCAC TCGACGTTTC GGAGGCCTAT ATGGAAATGG TCGATAATAT
M H W V R Q A P G Q G L E W M G W
BstXI
XhoI
TGCACTGGGT CCGCCAAGCC CCTGGGCAGG GTCTCGAGTG GATGGGCTGG
ACGTGACCCA GGCGGTTCGG GGACCCGTCC CAGAGCTCAC CTACCCGACC

FIG. 5D

```
 I  N  P  N   S  G  G   T  N  Y   A  Q  K  F   Q  G  R
ATTAACCCGA ATAGCGGCGG CACGAACTAC GCGCAGAAGT TTCAGGGCCG
TAATTGGGCT TATCGCCGCC GTGCTTGATG CGCGTCTTCA AAGTCCCGGC


  V  T  M   T  R  D  T   S  I  S   T  A  Y   M  E  L
BstEII
~~~~~~~
GGTGACCATG ACCCGTGATA CCAGCATTAG CACCGCGTAT ATGGAACTGA
CCACTGGTAC TGGGCACTAT GGTCGTAATC GTGGCGCATA TACCTTGACT

S  S  L  R   S  E  D   T  A  V  Y   Y  C  A   R  W  G
                      EagI           BssHII
                      ~~~~~~         ~~~~~~~
GCAGCCTGCG TAGCGAAGAT ACGGCCGTGT ATTATTGCGC GCGTTGGGGC
CGTCGGACGC ATCGCTTCTA TGCCGGCACA TAATAACGCG CGCAACCCCG
```

FIG. 5E

```
  G   D   G   F     Y   A   M     D   Y   W     G   Q   G   T     L   V   T
                                                    StyI
                                                  ~~~~~~~
GGCGATGGCT TTTATGCGAT GGATTATTGG GGCCAAGGCA CCCTGGTGAC
CCGCTACCGA AAATACGCTA CCTAATAACC CCGGTTCCGT GGGACCACTG

  V   S   S
      BlpI
    ~~~~~~
GGTTAGCTCA G
CCAATCGAGT C
```

FIG. 5F

```
 Q  V  Q  L  K  E  S  G  P  A  L  V  K  P  T  Q  T
       MfeI
      ~~~~~~~
CAGGTGCAAT TGAAAGAAAG CGGCCCGGCC CTGGTGAAAC CGACCCAAAC
GTCCACGTTA ACTTTCTTTC GCCGGGCCGG GACCACTTTG GCTGGGTTTG

  L  T  L  T  C  T  F  S  G  F  S  L  S  T  S  G
                      BspEI
                     ~~~~~~
CCTGACCCTG ACCTGTACCT TTTCCGGATT TAGCCTGTCC ACGTCTGGCG
GGACTGGGAC TGGACATGGA AAAGGCCTAA ATCGGACAGG TGCAGACCGC

V  G  V  G  W  I  R  Q  P  P  G  K  A  L  E  W  L
                      BstXI              XhoI
                  ~~~~~~~~~~~~~~     ~~~~~~~
TTGGCGTGGG CTGGATTCGC CAGCCGCCTG GGAAAGCCCT CGAGTGGCTG
AACCGCACCC GACCTAAGCG GTCGGCGGAC CCTTTCGGGA GCTCACCGAC
```

FIG. 5G

```
 A   L   I   D    W   D   D    D   K   Y    Y   S   T   S    L   K   T
                                                            MluI
                                                             ~~
GCTCTGATTG ATTGGGATGA TGATAAGTAT TATAGCACCA GCCTGAAAAC
CGAGACTAAC TAACCCTACT ACTATTCATA ATATCGTGGT CGGACTTTTG

  R   L   T    I   S   K   D    T   S   K    N   Q   V    V   L   T
MluI                          NspV
~~~~                          ~~~~~~
GCGTCTGACC ATTAGCAAAG ATACTTCGAA AAATCAGGTG GTGCTGACTA
CGCAGACTGG TAATCGTTTC TATGAAGCTT TTTAGTCCAC CACGACTGAT

M   T   N   M    D   P   V    D   T   A   T    Y   Y   C    A   R   W
                                                    BssHII
                                                    ~~~~~~~
TGACCAACAT GGACCCGGTG GATACGGCCA CCTATTATTG CGCGCGTTGG
ACTGGTTGTA CCTGGGCCAC CTATGCCGGT GGATAATAAC GCGCGCAACC
```

FIG. 5H

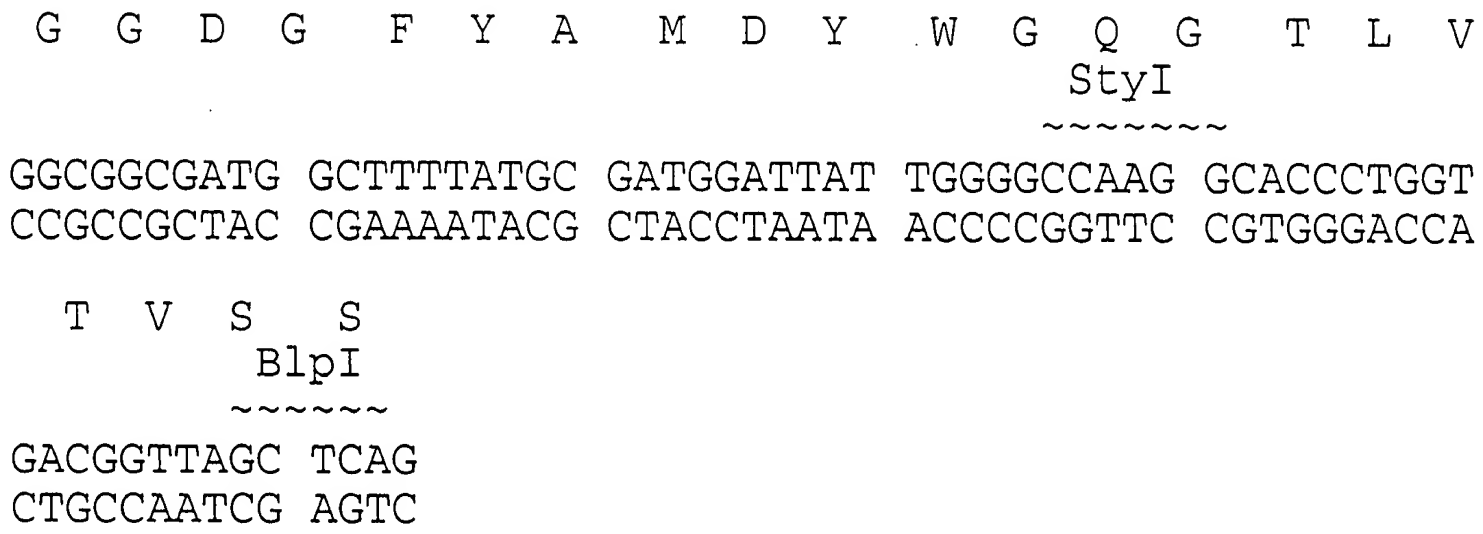

G G D G F Y A M D Y W G Q G T L V
StyI
GGCGGCGATG GCTTTTATGC GATGGATTAT TGGGGCCAAG GCACCCTGGT
CCGCCGCTAC CGAAAATACG CTACCTAATA ACCCCGGTTC CGTGGGACCA
T V S S
BlpI
GACGGTTAGC TCAG
CTGCCAATCG AGTC

FIG. 5I

```
 E  V  Q  L     V  E  S     G  G  G     L  V  Q  P     G  G  S
       MfeI
     ~~~~~~~
GAAGTGCAAT TGGTGGAAAG CGGCGGCGGC CTGGTGCAAC CGGGCGGCAG
CTTCACGTTA ACCACCTTTC GCCGCCGCCG GACCACGTTG GCCCGCCGTC

  L  R  L     S  C  A  A     S  G  F     T  F  S     S  Y  A
                            BspEI
                          ~~~~~~
CCTGCGTCTG AGCTGCGCGG CCTCCGGATT TACCTTTAGC AGCTATGCGA
GGACGCAGAC TCGACGCGCC GGAGGCCTAA ATGGAAATCG TCGATACGCT

M  S  W  V     R  Q  A     P  G  K  G     L  E  W     V  S  A
                  BstXI                    XhoI
               ~~~~~~~~~~~~~~          ~~~~~~
TGAGCTGGGT GCGCCAAGCC CCTGGGAAGG GTCTCGAGTG GGTGAGCGCG
ACTCGACCCA CGCGGTTCGG GGACCCTTCC CAGAGCTCAC CCACTCGCGC
```

FIG. 5J

```
 I  S  G  S   G  G  S   T  Y  Y   A  D  S  V   K  G  R
ATTAGCGGTA GCGGCGGCAG CACCTATTAT GCGGATAGCG TGAAAGGCCG
TAATCGCCAT CGCCGCCGTC GTGGATAATA CGCCTATCGC ACTTTCCGGC

 F  T  I   S  R  D  N   S  K  N   T  L  Y   L  Q  M
             PmlI       NspV
            ~~~~~~     ~~~~~~
TTTTACCATT TCACGTGATA ATTCGAAAAA CACCCTGTAT CTGCAAATGA
AAAATGGTAA AGTGCACTAT TAAGCTTTTT GTGGGACATA GACGTTTACT

N  S  L  R   A  E  D   T  A  V  Y   Y  C  A   R  W  G
                       EagI          BssHII
                      ~~~~~~        ~~~~~~~
ACAGCCTGCG TGCGGAAGAT ACGGCCGTGT ATTATTGCGC GCGTTGGGGC
TGTCGGACGC ACGCCTTCTA TGCCGGCACA TAATAACGCG CGCAACCCCG
```

FIG. 5K

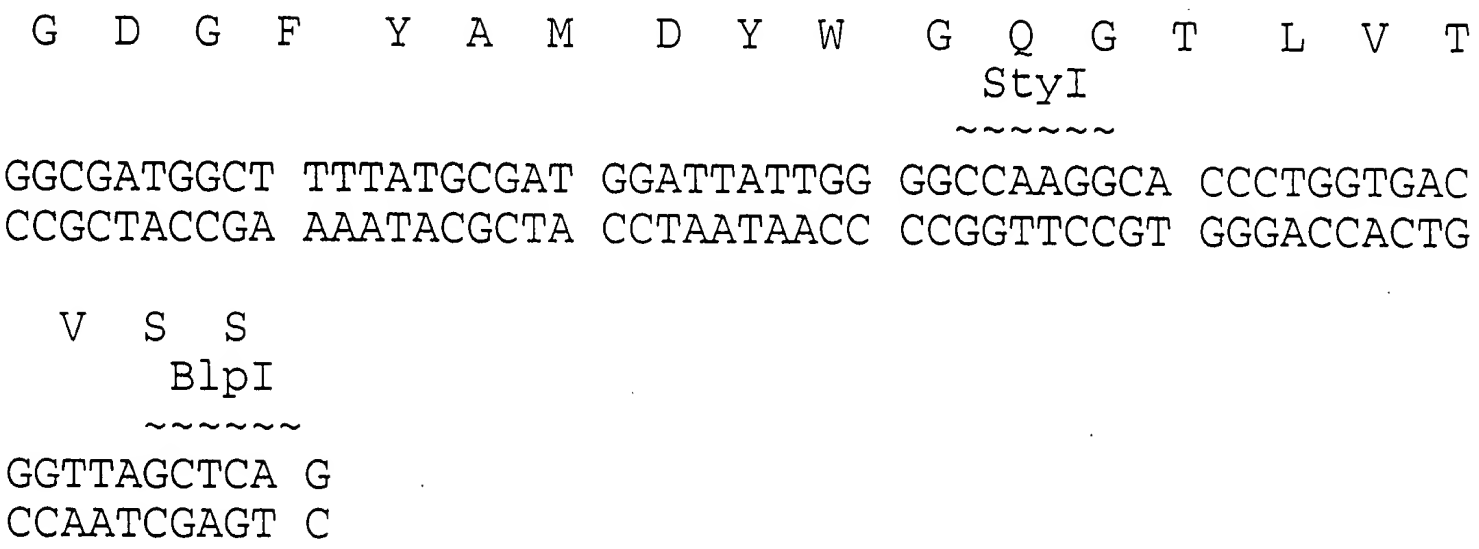

G D G F Y A M D Y W G Q G T L V T
StyI
GGCGATGGCT TTTATGCGAT GGATTATTGG GGCCAAGGCA CCCTGGTGAC
CCGCTACCGA AAATACGCTA CCTAATAACC CCGGTTCCGT GGGACCACTG
V S S
BlpI
GGTTAGCTCA G
CCAATCGAGT C

FIG. 5L

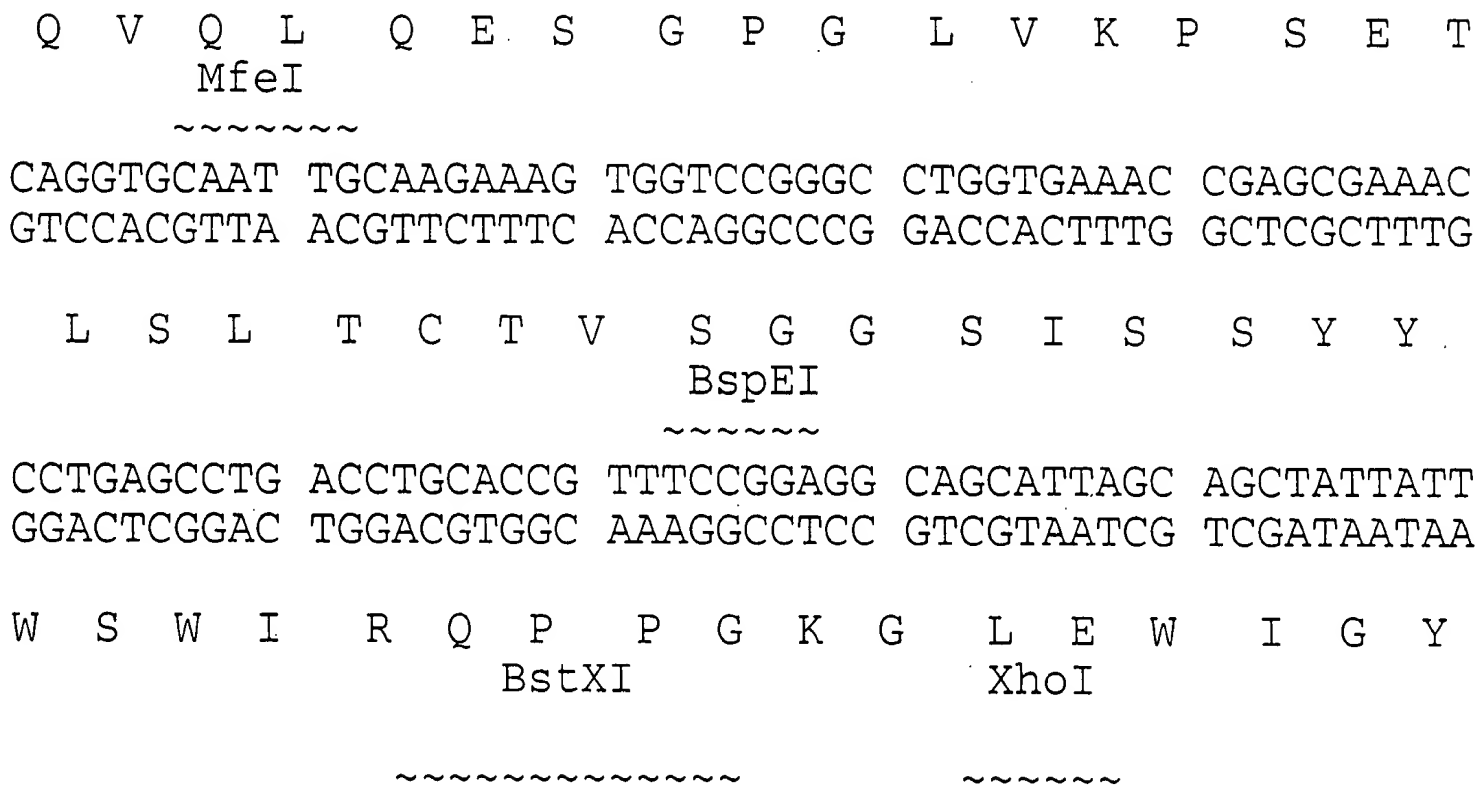

Q V Q L Q E S G P G L V K P S E T
MfeI
CAGGTGCAAT TGCAAGAAAG TGGTCCGGGC CTGGTGAAAC CGAGCGAAAC
GTCCACGTTA ACGTTCTTTC ACCAGGCCCG GACCACTTTG GCTCGCTTTG
L S L T C T V S G G S I S S Y Y
BspEI
CCTGAGCCTG ACCTGCACCG TTTCCGGAGG CAGCATTAGC AGCTATTATT
GGACTCGGAC TGGACGTGGC AAAGGCCTCC GTCGTAATCG TCGATAATAA
W S W I R Q P P G K G L E W I G Y
BstXI
XhoI

FIG. 5M

```
GGAGCTGGAT TCGCCAGCCG CCTGGGAAGG GTCTCGAGTG GATTGGCTAT
CCTCGACCTA AGCGGTCGGC GGACCCTTCC CAGAGCTCAC CTAACCGATA

 I  Y  Y  S   G  S  T   N  Y  N   P  S  L  K   S  R  V
                                                BstEII
                                                ~~~
ATTTATTATA GCGGCAGCAC CAACTATAAT CCGAGCCTGA AAAGCCGGGT
TAAATAATAT CGCCGTCGTG GTTGATATTA GGCTCGGACT TTTCGGCCCA

  T  I  S   V  D  T  S   K  N  Q   F  S  L  K   L  S
BstEII          NspV
~~~~            ~~~~~~~
GACCATTAGC GTTGATACTT CGAAAAACCA GTTTAGCCTG AAACTGAGCA
CTGGTAATCG CAACTATGAA GCTTTTTGGT CAAATCGGAC TTTGACTCGT

S  V  T  A   A  D  T   A  V  Y  Y   C  A  R   W  G  G
                EagI                BssHII
                ~~~~~~~             ~~~~~~
```

FIG. 5N

```
GCGTGACGGC GGCGGATACG GCCGTGTATT ATTGCGCGCG TTGGGGCGGC
CGCACTGCCG CCGCCTATGC CGGCACATAA TAACGCGCGC AACCCCGCCG

 D  G  F  Y  A  M  D  Y  W  G  Q  G  T  L  V  T  V
                              StyI
                           ~~~~~~~
GATGGCTTTT ATGCGATGGA TTATTGGGGC CAAGGCACCC TGGTGACGGT
CTACCGAAAA TACGCTACCT AATAACCCCG GTTCCGTGGG ACCACTGCCA

  S  S
   BlpI
  ~~~~~
TAGCTCAG
ATCGAGTC
```

FIG. 5O

```
 E  V  Q  L  V  Q  S  G  A  E  V  K  K  P  G  E  S
       MfeI
     ~~~~~~~
GAAGTGCAAT TGGTTCAGAG CGGCGCGGAA GTGAAAAAAC CGGGCGAAAG
CTTCACGTTA ACCAAGTCTC GCCGCGCCTT CACTTTTTTG GCCCGCTTTC

  L  K  I  S  C  K  G  S  G  Y  S  F  T  S  Y  W
                      BspEI
                    ~~~~~~
CCTGAAAATT AGCTGCAAAG GTTCCGGATA TTCCTTTACG AGCTATTGGA
GGACTTTTAA TCGACGTTTC CAAGGCCTAT AAGGAAATGC TCGATAACCT

I  G  W  V  R  Q  M  P  G  K  G  L  E  W  M  G  I
               BstXI              XhoI
            ~~~~~~~~~~~~~      ~~~~~~
TTGGCTGGGT GCGCCAGATG CCTGGGAAGG GTCTCGAGTG GATGGGCATT
AACCGACCCA CGCGGTCTAC GGACCCTTCC CAGAGCTCAC CTACCCGTAA
```

FIG. 5P

```
 I   Y   P   G    D   S   D    T   R   Y    S   P   S   F    Q   G   Q
ATTTATCCGG GCGATAGCGA TACCCGTTAT TCTCCGAGCT TTCAGGGCCA
TAAATAGGCC CGCTATCGCT ATGGGCAATA AGAGGCTCGA AAGTCCCGGT

  V   T   I    S   A   D   K    S   I   S    T   A   Y    L   Q   W
BstEII
~~~~~~~
GGTGACCATT AGCGCGGATA AAAGCATTAG CACCGCGTAT CTTCAATGGA
CCACTGGTAA TCGCGCCTAT TTTCGTAATC GTGGCGCATA GAAGTTACCT

S   S   L   K    A   S   D    T   A   M   Y    Y   C   A    R   W   G
                                              BssHII
                                              ~~~~~~~
GCAGCCTGAA AGCGAGCGAT ACGGCCATGT ATTATTGCGC GCGTTGGGGC
CGTCGGACTT TCGCTCGCTA TGCCGGTACA TAATAACGCG CGCAACCCCG
```

FIG.5Q

```
 G  D  G  F   Y  A  M   D  Y  W   G  Q  G  T   L  V  T
                                    StyI
                                   ~~~~~~
GGCGATGGCT TTTATGCGAT GGATTATTGG GGCCAAGGCA CCCTGGTGAC
CCGCTACCGA AAATACGCTA CCTAATAACC CCGGTTCCGT GGGACCACTG

  V  S  S
     BlpI
    ~~~~~~
GGTTAGCTCA G
CCAATCGAGT C
```

FIG.5R

```
 Q  V  Q  L   Q  Q  S   G  P  G   L  V  K  P   S  Q  T
       MfeI
      ~~~~~~~
CAGGTGCAAT TGCAACAGTC TGGTCCGGGC CTGGTGAAAC CGAGCCAAAC
GTCCACGTTA ACGTTGTCAG ACCAGGCCCG GACCACTTTG GCTCGGTTTG

  L  S  L   T  C  A  I   S  G  D   S  V  S   S  N  S
                        BspEI
                       ~~~~~~
CCTGAGCCTG ACCTGTGCGA TTTCCGGAGA TAGCGTGAGC AGCAACAGCG
GGACTCGGAC TGGACACGCT AAAGGCCTCT ATCGCACTCG TCGTTGTCGC

A  A  W  N   W  I  R   Q  S  P  G   R  G  L   E  W  L
                        BstXI          XhoI
                  ~~~~~~~~~~~~~~~     ~~~~~~~
CGGCGTGGAA CTGGATTCGC CAGTCTCCTG GGCGTGGCCT CGAGTGGCTG
GCCGCACCTT GACCTAAGCG GTCAGAGGAC CCGCACCGGA GCTCACCGAC
```

FIG.5S

```
 G  R  T  Y   Y  R  S   K  W  Y   N  D  Y  A   V  S  V
GGCCGTACCT ATTATCGTAG CAAATGGTAT AACGATTATG CGGTGAGCGT
CCGGCATGGA TAATAGCATC GTTTACCATA TTGCTAATAC GCCACTCGCA

 K  S  R   I  T  I  N   P  D  T   S  K  N   Q  F  S
          BsaBI                  NspV
       ~~~~~~~~~~~            ~~~~~~
GAAAAGCCGG ATTACCATCA ACCCGGATAC TTCGAAAAAC CAGTTTAGCC
CTTTTCGGCC TAATGGTAGT TGGGCCTATG AAGCTTTTTG GTCAAATCGG

L  Q  L  N   S  V  T   P  E  D  T   A  V  Y   Y  C  A
                                   EagI          BssHII
                                  ~~~~~~         ~~~~~
TGCAACTGAA CAGCGTGACC CCGGAAGATA CGGCCGTGTA TTATTGCGCG
ACGTTGACTT GTCGCACTGG GGCCTTCTAT GCCGGCACAT AATAACGCGC
```

FIG. 5T

```
 R  W  G  G   D  G  F   Y  A  M   D  Y  W  G   Q  G  T
BssHII                                          StyI
~                                               ~~~~~~~
CGTTGGGGCG GCGATGGCTT TTATGCGATG GATTATTGGG GCCAAGGCAC
GCAACCCCGC CGCTACCGAA AATACGCTAC CTAATAACCC CGGTTCCGTG

  L  V  T   V  S  S
                BlpI
               ~~~~~~~
CCTGGTGACG GTTAGCTCAG
GGACCACTGC CAATCGAGTC
```

FIG. 5U

O1K1 5'- GAATGCATACGCTGATATCCAGATGACCCAGAG-
CCCGTCTAGCCTGAGC -3'

O1K2 5'- CGCTCTGCAGGTAATGGTCACACGATCACCCAC-
GCTCGCGCTCAGGCTAGACGGGC -3'

O1K3 5'- GACCATTACCTGCAGAGCGAGCCAGGGCATTAG-
CAGCTATCTGGCGTGGTACCAGCAG -3'

O1K4 5'- CTTTGCAAGCTGCTGGCTGCATAAATTAATAGT-
TTCGGTGCTTTACCTGGTTTCTGCTGGTACCACGCCAG -3'

O1K5 5'- CAGCCAGCAGCTTGCAAAGCGGGGTCCCGTCCC-
GTTTTAGCGGCTCTGGATCCGGCACTGATTTTAC -3'

O1K6 5'- GATAATAGGTCGCAAAGTCTTCAGGTTGCAGGC-
TGCTAATGGTCAGGGTAAAATCAGTGCCGGATCC -3'

O2K1 5'- CGATATCGTGATGACCCAGAGCCCACTGAGCCT-
GCCAGTGACTCCGGGCGAGCC -3'

O2K2 5'- GCCGTTGCTATGCAGCAGGCTTTGGCTGCTTCT-
GCAGCTAATGCTCGCAGGCTCGCCCGGAGTCAC -3'

O2K3 5'- CTGCTGCATAGCAACGGCTATAACTATCTGGAT-
TGGTACCTTCAAAAACCAGGTCAAAGCCC -3'

O2K4 5'- CGATCCGGGACCCCACTGGCACGGTTGCTGCCC-
AGATAAATTAATAGCTGCGGGCTTTGACCTGGTTTTTG -3'

O2K5 5'- AGTGGGGTCCCGGATCGTTTTAGCGGCTCTGGA-
TCCGGCACCGATTTTACCCTGAAAATTAGCCGTGTG -3'

O2K6 5'- CCATGCAATAATACACGCCCACGTCTTCAGCTT-
CCACACGGCTAATTTTCAGGG -3'

O3K1 5'- GAATGCATACGCTGATATCGTGCTGACCCAGAG
CCCGG -3'

O3K2 5'- CGCTCTGCAGCTCAGGGTCGCACGTTCGCCCGG-
AGACAGGCTCAGGGTCGCCGGGCTCTGGGTCAGC -3'

O3K3 5'- CCCTGAGCTGCAGAGCGAGCCAGAGCGTGAGCA-
GCAGCTATCTGGCGTGGTACCAG -3'

FIG. 6A

O3K4 5'- GCACGGCTGCTCGCGCCATAAATTAATAGACGC-
GGTGCTTGACCTGGTTTCTGCTGGTACCACGCCAGATAG -3'

O3K5 5'- GCGCGAGCAGCCGTGCAACTGGGGTCCCGGCGC-
GTTTTAGCGGCTCTGGATCCGGCACGGATTTTAC -3'

O3K6 5'- GATAATACACCGCAAAGTCTTCAGGTTCCAGGC-
TGCTAATGGTCAGGGTAAAATCCGTGCCGGATC -3'

O4K1 5'- GAATGCATACGCTGATATCGTGATGACCCAGAG-
CCCGGATAGCCTGGCG -3'

O4K2 5'- GCTTCTGCAGTTAATGGTCGCACGTTCGCCCAG-
GCTCACCGCCAGGCTATCCGGGC -3'

O4K3 5'- CGACCATTAACTGCAGAAGCAGCCAGAGCGTGC-
TGTATAGCAGCAACAACAAAAACTATCTGGCGTGGTACCAG
3'

O4K4 5'- GATGCCCAATAAATTAATAGTTTCGGCGGCTGA-
CCTGGTTTCTGCTGGTACCACGCCAGATAG -3'

O4K5 5'- AAACTATTAATTTATTGGGCATCCACCCGTGAA-
AGCGGGGTCCCGGATCGTTTTAGCGGCTCTGGATCCGGCAC-
3'

O4K6 5'- GATAATACACCGCCACGTCTTCAGCTTGCAGGG-
ACGAAATGGTCAGGGTAAAATCAGTGCCGGATCCAGAGCC-
3'

O1L1 5'- GAATGCATACGCTCAGAGCGTGCTGACCCAGCC-
GCCTTCAGTGAGTGG -3'

O1L2 5'- CAATGTTGCTGCTGCTGCCGCTACACGAGATGG-
TCACACGCTGACCTGGTGCGCCACTCACTGAAGGCGGC -3'

O1L3 5'- GGCAGCAGCAGCAACATTGGCAGCAACTATGTG-
AGCTGGTACCAGCAGTTGCCCGGGAC -3'

O1L4 5'- CCGGCACGCCTGAGGGACGCTGGTTGTTATCAT-
AAATCAGCAGTTTCGGCGCCGTCCCGGGCAACTGC -3
O1L5 5'- CCCTCAGGCGTGCCGGATCGTTTTAGCGGATCC-
AAAAGCGGCACCAGCGCGAGCCTTGCG -3'

FIG.6B

O1L6 5'- CCGCTTCGTCTTCGCTTTGCAGGCCCGTAATCG-
CAAGGCTCGCGCTGG -3'
O2L1 5'- GAATGCATACGCTCAGAGCGCACTGACCCAGCC-
AGCTTCAGTGAGCGGC -3'
O2L2 5'- CGCTGCTAGTACCCGTACACGAGATGGTAATGC-
TCTGACCTGGTGAGCCGCTCACTGAAGCTGG -3'
O2L3 5'- GTACGGGTACTAGCAGCGATGTGGGCGGCTATA-
ACTATGTGAGCTGGTACCAGCAGCATCCCGG -3'
O2L4 5'- CGCCTGAGGGACGGTTGCTCACATCATAAATCA-
TCAGTTTCGGCGCCTTCCCGGGATGCTGCTGGTAC -3'
O2L5 5'- CAACCGTCCCTCAGGCGTGAGCAACCGTTTTAG-
CGGATCCAAAAGCGGCAACACCGCGAGCC -3'
O2L6 5'- CCGCTTCGTCTTCCGCTTGCAGGCCGCTAATGG-
TCAGGCTCGCGGTGTTGCCG -3'
O3L1 5'- GAATGCATACGCTAGCTATGAACTGACCCAGCC-
GCCTTCAGTGAGCG -3'
O3L2 5'- CGCCCAGCGCATCGCCGCTACACGAGATACGCG-
CGGTCTGACCTGGTGCAACGCTCACTGAAGGCGGC -3'
O3L3 5'- GGCGATGCGCTGGGCGATAAATACGCGAGCTGG-
TACCAGCAGAAACCCGGGCAGGCGC -3'
O3L4 5'- GCGTTCCGGGATGCCTGAGGGACGGTCAGAATC-
ATCATAAATCACCAGAACTGGCGCCTGCCCGGGTTTC -3'
O3L5 5'- CAGGCATCCCGGAACGCTTTAGCGGATCCAACA-
GCGGCAACACCGCGACCCTGACCATTAGCGG -3'
O3L6 5'- CCGCTTCGTCTTCCGCCTGAGTGCCGCTAATGG-
TCAGGGTC -3'
O1246H1 5'- GCTCTTCACCCCTGTTACCAAAGCCCAG-
GTGCAATTG -3'
O1AH25'- GGCTTTGCAGCTCACTTTCACGCTGCTGCCCGGT-
TTTTTCACTTCCGCGCCAGACTGAACCAATTGCACCTGGGC-
TTTG -3'

FIG. 6C

O1AH3 5'- GAAAGTGAGCTGCAAAGCCTCCGGAGGCACTTT-
TAGCAGCTATGCGATTAGCTGGGTGCGCCAAGCCCCTGGGCAG
GGTC -3'
O1AH4 5'- GCCCTGAAACTTCTGCGCGTAGTTCGCCGTGCCA-
AAAATCGGAATAATGCCGCCCATCCACTCGAGACCCTGCCC-
AGGGGC -3'
O1AH5 5'- GCGCAGAAGTTTCAGGGCCGGGTGACCATTACC-
GCGGATGAAAGCACCAGCACCGCGTATATGGAACTGAGCAGCC
TGCG -3'
O1ABH6 5'- GCGCGCAATAATACACGGCCGTATCTTCGCT-
ACGCAGGCTGCTCAGTTCC -3'
O1BH2 5'- GGCTTTGCAGCTCACTTTCACGCTCGCGCCCGGT-
TTTTTCACTTCCGCGCCGCTCTGAACCAATTGCACCTGGGC-
TTTG -3'
O1BH3 5'- GAAAGTGAGCTGCAAAGCCTCCGGATATACCTT-
TACCAGCTATTATATGCACTGGGTCCGCCAAGCCCCTGGGCAG
GGTC -3'
O1BH4 5'- GCCCTGAAACTTCTGCGCGTAGTTCGTGCCGCC-
GCTATTCGGGTTAATCCAGCCCATCCACTCGAGACCCTGCCCA
GGGGC -3'
O1BH5 5'- GCGCAGAAGTTTCAGGGCCGGGTGACCATGACC-
CGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCAGCC
TGCG -3'
O2H2 5'- GGTACAGGTCAGGGTCAGGGTTTGGGTCGGTTT-
CACCAGGGCCGGGCCGCTTTCTTTCAATTGCACCTGGGCTTTG
-3'
O2H3 5'- CTGACCCTGACCTGTACCTTTTCCGGATTTAGC-
CTGTCCACGTCTGGCGTTGGCGTGGGCTGGATTCGCCAGCCGC
CTGGGAAAG -3
O2H4 5'- GCGTTTTCAGGCTGGTGCTATAATACTTATCAT-
CATCCCAATCAATCAGAGCCAGCCACTCGAGGGCTTTCCCAGG
CGGCTGG -3'

FIG. 6D

O2H5 5'- GCACCAGCCTGAAAACGCGTCTGACCATTAGCA-
AAGATACTTCGAAAAATCAGGTGGTGCTGACTATGACCAACAT
GG -3'
O2H6 5'- GCGCGCAATAATAGGTGGCCGTATCCACCGGGT-
CCATGTTGGTCATAGTCAGC -3'
O3H1 5'- CGAAGTGCAATTGGTGGAAAGCGGCGGCGGCCT-
GGTGCAACCGGGCGGCAG -3'
O3H2 5'- CATAGCTGCTAAAGGTAAATCCGGAGGCCGCGC-
AGCTCAGACGCAGGCTGCCGCCCGGTTGCAC -3'
O3H3 5'- GATTTACCTTTAGCAGCTATGCGATGAGCTGGG-
TGCGCCAAGCCCCTGGGAAGGGTCTCGAGTGGGTGAG -3'
O3H4 5'- GGCCTTTCACGCTATCCGCATAATAGGTGCTGC-
CGCCGCTACCGCTAATCGCGCTCACCCACTCGAGACCC -3'
O3H5 5'- CGGATAGCGTGAAAGGCCGTTTTACCATTTCAC-
GTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAG-3'
O3H6 5'- CACGCGCGCAATAATACACGGCCGTATCTTCCG-
CACGCAGGCTGTTCATTTGCAGATACAGG -3'
O4H2 5'- GGTCAGGCTCAGGGTTTCGCTCGGTTTCACCAG-
GCCCGGACCACTTTCTTGCAATTGCACCTGGGCTTTG -3'
O4H3 5'- GAAACCCTGAGCCTGACCTGCACCGTTTCCGGAGG-
CAGCATTAGCAGCTATTATTGGAGCTGGATTCGCCAGCCGC
-3'
O4H4 5'- GATTATAGTTGGTGCTGCCGCTATAATAAATAT-
AGCCAATCCACTCGAGACCCTTCCCAGGCGGCTGGCGAATCCA
G -3'
O4H5 5'- CGGCAGCACCAACTATAATCCGAGCCTGAAAAG-
CCGGGTGACCATTAGCGTTGATACTTCGAAAAACCAGTTTAGC
CTG -3'
O4H6 5'- GCGCGCAATAATACACGGCCGTATCCGCCGCCG-
TCACGCTGCTCAGTTTCAGGCTAAACTGGTTTTTCG -3'

FIG. 6E

O5H1 5'- GCTCTTCACCCCTGTTACCAAAGCCGAAGTGCA
ATTG -3'
O5H2 5'- CCTTTGCAGCTAATTTTCAGGCTTTCGCCCGGT-
TTTTTCACTTCCGCGCCGCTCTGAACCAATTGCACTTCGGCTT
TGG -3'
O5H3 5'- CCTGAAAATTAGCTGCAAAGGTTCCGGATATTC-
CTTTACGAGCTATTGGATTGGCTGGGTGCGCCAGATGCCTGG
-3'
O5H4 5'- CGGAGAATAACGGGTATCGCTATCGCCCGGATA-
AATAATGCCCATCCACTCGAGACCCTTCCCAGGCATCTGGCGC
AC -3'
O5H5 5'- CGATACCCGTTATTCTCCGAGCTTTCAGGGCCA-
GGTGACCATTAGCGCGGATAAAAGCATTAGCACCGCGTATCTT
C -3'
O5H6 5'- GCGCGCAATAATACATGGCCGTATCGCTCGCTT-
TCAGGCTGCTCCATTGAAGATACGCGGTGCTAATG -3'
O6H2 5'- GAAATCGCACAGGTCAGGCTCAGGGTTTGGCTC-
GGTTTCACCAGGCCCGGACCAGACTGTTGCAATTGCACCTGG-
GCTTTG -3'
O6H3 5'- GCCTGACCTGTGCGATTTCCGGAGATAGCGTGA-
GCAGCAACAGCGCGGCGTGGAACTGGATTCGCCAGTCTCCTGG
GCG -3'
O6H4 5'- CACCGCATAATCGTTATACCATTTGCTACGATA-
ATAGGTACGGCCCAGCCACTCGAGGCCACGCCCAGGAGACTG
GCG -3'
O6H5 5'- GGTATAACGATTATGCGGTGAGCGTGAAAAGCC-
GGATTACCATCAACCCGGATACTTCGAAAAACCAGTTTAGCCT
GC -3'
O6H6 5'- GCGCGCAATAATACACGGCCGTATCTTCCGGGG-
TCACGCTGTTCAGTTGCAGGCTAAACTGGTTTTTC -3'
OCLK1 5'- GGCTGAAGACGTGGGCGTGTATTATTGCCAGCA-
GCATTATACCACCCCGCCGACCTTTGGCCAGGGTAC -3'

FIG. 6F

OCLK2 5'- GCGAAAAATAAACACGCTCGGAGCAGCCACCG-
TACGTTTAATTTCAACTTTCGTACCCTGGCCAAAGGTC -3'
OCLK3 5'- GAGCGTGTTTATTTTTCCGCCGAGCGATGAACA-
ACTGAAAAGCGGCACGGCGAGCGTGGTGTGCCTGCTG -3'
OCLK4 5'- CAGCGCGTTGTCTACTTTCCACTGAACTTTCGC-
TTCACGCGGATAAAAGTTGTTCAGCAGGCACACCACGC -3'
OCLK5 5'- GAAAGTAGACAACGCGCTGCAAAGCGGCAACAG-
CCAGGAAAGCGTGACCGAACAGGATAGCAAAGATAG -3'
OCLK6 5'- GTTTTTCATAATCCGCTTTGCTCAGGGTCAGGG-
TGCTGCTCAGAGAATAGGTGCTATCTTTGCTATCCTGTTCG -
3'
OCLK7 5'- GCAAAGCGGATTATGAAAAACATAAAGTGTATG-
CGTGCGAAGTGACCCATCAAGGTCTGAGCAGCCCGGTG -3'
OCLK8 5'- GGCATGCTTATCAGGCCTCGCCACGATTAAAAG-
ATTTAGTCACCGGGCTGCTCAGAC -3'
OCH1 5'- GGCGTCTAGAGGCCAAGGCACCCTGGTGACGGT-
TAGCTCAGCGTCGAC -3'
OCH2 5'- GTGCTTTTGCTGCTCGGAGCCAGCGGAAACACG-
CTTGGACCTTTGGTCGACGCTGAGCTAACC -3'
OCH3 5'- CTCCGAGCAGCAAAAGCACCAGCGGCGGCACGG-
CTGCCCTGGGCTGCCTGGTTAAAGATTATTTCC -3'
OCH4 5'- CTGGTCAGCGCCCCGCTGTTCCAGCTCACGGTG-
ACTGGTTCCGGGAAATAATCTTTAACCAGGCA -3'
OCH5 5'- AGCGGGGCGCTGACCAGCGGCGTGCATACCTTT-
CCGGCGGTGCTGCAAAGCAGCGGCCTG -3'
OCH6 5'- GTGCCTAAGCTGCTGCTCGGCACGGTCACAACG-
CTGCTCAGGCTATACAGGCCGCTGCTTTGCAG -3'
OCH7 5'- GAGCAGCAGCTTAGGCACTCAGACCTATATTTG-
CAACGTGAACCATAAACCGAGCAACACC -3'
OCH8 5'- GCGCGAATTCGCTTTTCGGTTCCACTTTTTTAT-
CCACTTTGGTGTTGCTCGGTTTATGG -3'

FIG. 6G

```
      V  A   A  P  S   V  F  I   F  P  P  S   D  E  Q
 BsiWI
~~~~~~
CGTACGGTGG CTGCTCCGAG CGTGTTTATT TTTCCGCCGA GCGATGAACA
GCATGCCACC GACGAGGCTC GCACAAATAA AAAGGCGGCT CGCTACTTGT

  L  K  S   G  T  A  S   V  V  C   L  L  N   N  F  Y
ACTGAAAAGC GGCACGGCGA GCGTGGTGTG CCTGCTGAAC AACTTTTATC
TGACTTTTCG CCGTGCCGCT CGCACCACAC GGACGACTTG TTGAAAATAG

P  R  E  A   K  V  Q   W  K  V  D   N  A  L   Q  S  G
CGCGTGAAGC GAAAGTTCAG TGGAAAGTAG ACAACGCGCT GCAAAGCGGC
GCGCACTTCG CTTTCAAGTC ACCTTTCATC TGTTGCGCGA CGTTTCGCCG

 N  S  Q  E   S  V  T   E  Q  D   S  K  D  S   T  Y  S
AACAGCCAGG AAAGCGTGAC CGAACAGGAT AGCAAAGATA GCACCTATTC
TTGTCGGTCC TTTCGCACTG GCTTGTCCTA TCGTTTCTAT CGTGGATAAG
```

FIG. 7A

```
L  S  S  T  L  T  L  S  K  A  D  Y  E  K  H  K
TCTGAGCAGC ACCCTGACCC TGAGCAAAGC GGATTATGAA AAACATAAAG
AGACTCGTCG TGGGACTGGG ACTCGTTTCG CCTAATACTT TTTGTATTTC

V  Y  A  C  E  V  T  H  Q  G  L  S  S  P  V  T  K
TGTATGCGTG CGAAGTGACC CATCAAGGTC TGAGCAGCCC GGTGACTAAA
ACATACGCAC GCTTCACTGG GTAGTTCCAG ACTCGTCGGG CCACTGATTT

 S  F  N  R  G  E  A  *
                StuI        SphI
               ~~~~~~~     ~~~~~~
TCTTTTAATC GTGGCGAGGC CTGATAAGCA TGC
AGAAAATTAG CACCGCTCCG GACTATTCGT ACG
```

FIG. 7B

```
      A  S  T  K  G  P  S  V  F  P  L  A  P  S  S
 BlpI   SalI
~~~~~~~~~~~~~~~
GCTCAGCGTC GACCAAAGGT CCAAGCGTGT TTCCGCTGGC TCCGAGCAGC
CGAGTCGCAG CTGGTTTCCA GGTTCGCACA AAGGCGACCG AGGCTCGTCG

 K  S  T  S  G  G  T  A  A  L  G  C  L  V  K  D  Y
AAAAGCACCA GCGGCGGCAC GGCTGCCCTG GGCTGCCTGG TTAAAGATTA
TTTTCGTGGT CGCCGCCGTG CCGACGGGAC CCGACGGACC AATTTCTAAT

  F  P  E  P  V  T  V  S  W  N  S  G  A  L  T  S
TTTCCCGGAA CCAGTCACCG TGAGCTGGAA CAGCGGGGCG CTGACCAGCG
AAAGGGCCTT GGTCAGTGGC ACTCGACCTT GTCGCCCCGC GACTGGTCGC

G  V  H  T  F  P  A  V  L  Q  S  S  G  L  Y  S  L
GCGTGCATAC CTTTCCGGCG GTGCTGCAAA GCAGCGGCCT GTATAGCCTG
CGCACGTATG GAAAGGCCGC CACGACGTTT CGTCGCCGGA CATATCGGAC
```

FIG. 7C

```
 S  S  V  V  T  V  P  S  S  S  L  G  T  Q  T  Y  I
AGCAGCGTTG TGACCGTGCC GAGCAGCAGC TTAGGCACTC AGACCTATAT
TCGTCGCAAC ACTGGCACGG CTCGTCGTCG AATCCGTGAG TCTGGATATA

  C  N  V  N  H  K  P  S  N  T  K  V  D  K  K  V
TTGCAACGTG AACCATAAAC CGAGCAACAC CAAAGTGGAT AAAAAAGTGG
AACGTTGCAC TTGGTATTTG GCTCGTTGTG GTTTCACCTA TTTTTTCACC

E  P  K  S  E  F  *
           EcoRI    HindIII
           ~~~~~~    ~~~~~
AACCGAAAAG CGAATTCTGA TAAGCTT
TTGGCTTTTC GCTTAAGACT ATTCGAA
```

FIG. 7D

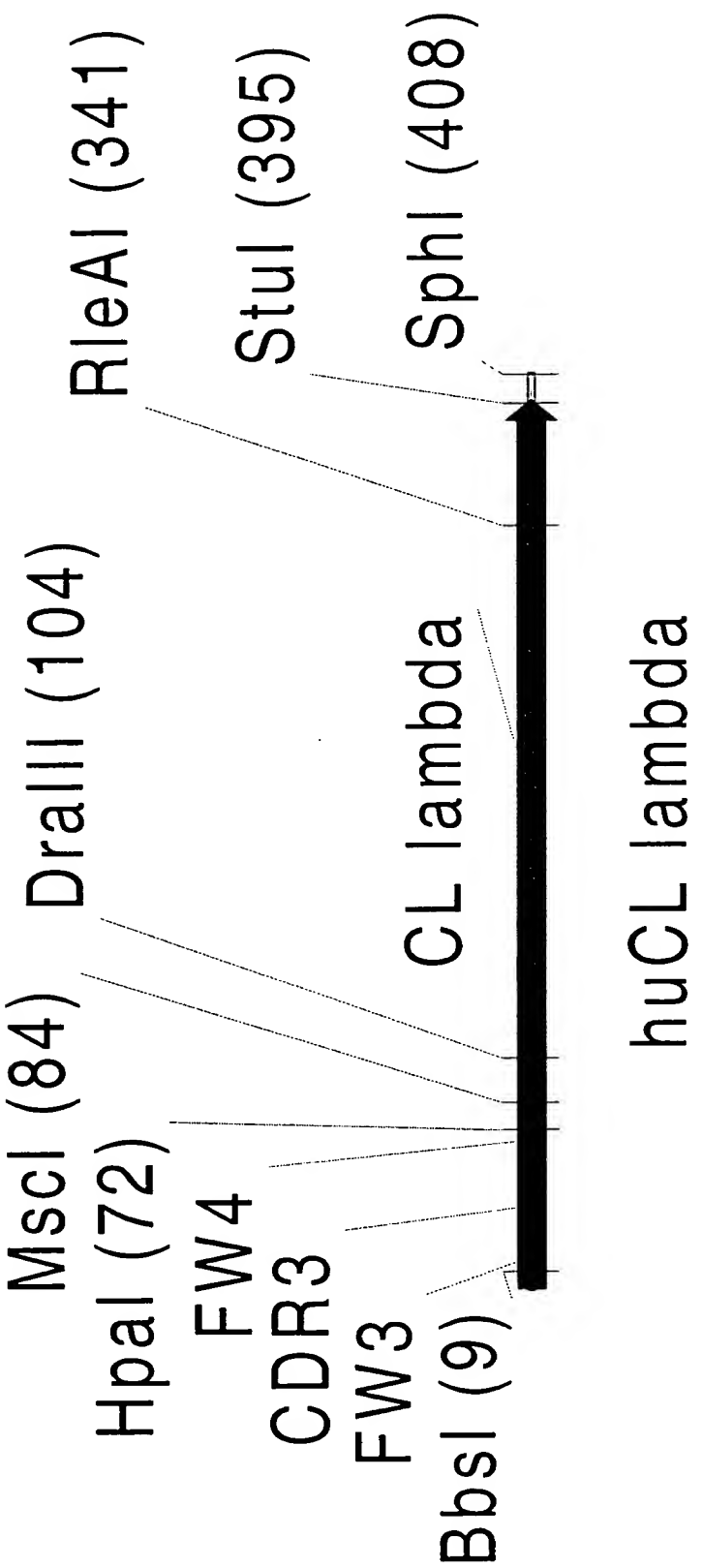

RleAI (341)
StuI (395)
SphI (408)
DraIII (104)
MscI (84)
HpaI (72)
FW4
CDR3
FW3
BbsI (9)
CL lambda
huCL lambda
408 bp

FIG. 7E

```
      BbsI
     ~~~~~~
  1  GAAGACGAAG CGGATTATTA TTGCCAGCAG CATTATACCA CCCCGCCTGT
     CTTCTGCTTC GCCTAATAAT AACGGTCGTC GTAATATGGT GGGGCGGACA

                           HpaI          MscI          DraIII
                          ~~~~~~~       ~~~~~~          ~~~
 51  GTTTGGCGGC GGCACGAAGT TAACCGTTCT TGGCCAGCCG AAAGCCGCAC
     CAAACCGCCG CCGTGCTTCA ATTGGCAAGA ACCGGTCGGC TTTCGGCGTG

     DraIII
     ~~~~~~
101  CGAGTGTGAC GCTGTTTCCG CCGAGCAGCG AAGAATTGCA GGCGAACAAA
     GCTCACACTG CGACAAAGGC GGCTCGTCGC TTCTTAACGT CCGCTTGTTT

151  GCGACCCTGG TGTGCCTGAT TAGCGACTTT TATCCGGGAG CCGTGACAGT
     CGCTGGGACC ACACGGACTA ATCGCTGAAA ATAGGCCCTC GGCACTGTCA
```

FIG. 7F

```
201  GGCCTGGAAG GCAGATAGCA GCCCCGTCAA GGCGGGAGTG GAGACCACCA
     CCGGACCTTC CGTCTATCGT CGGGGCAGTT CCGCCCTCAC CTCTGGTGGT

251  CACCCTCCAA ACAAAGCAAC AACAAGTACG CGGCCAGCAG CTATCTGAGC
     GTGGGAGGTT TGTTTCGTTG TTGTTCATGC GCCGGTCGTC GATAGACTCG

                              RleAI
                             ~~~~~~
301  CTGACGCCTG AGCAGTGGAA GTCCCACAGA AGCTACAGCT GCCAGGTCAC
     GACTGCGGAC TCGTCACCTT CAGGGTGTCT TCGATGTCGA CGGTCCAGTG

                                                  StuI
                                                 ~~~~~~~
```

FIG. 7G

```
351  GCATGAGGGG AGCACCGTGG AAAAAACCGT TGCGCCGACT GAGGCCTGAT
     CGTACTCCCC TCGTGGCACC TTTTTTGGCA ACGCGGCTGA CTCCGGACTA

        SphI
       ~~~~~
401  AAGCATGC
     TTCGTACG
```

FIG. 7H

M24: assembly PCR

M24-A:

GAAGACAAGCGGATTATTATTGCCAGCAGCATTATACCACCCCGCCTGTGTTTGGCGGCG-
GCACGAAGTTAACCGTTC

M24-B:

CAATTCTTCGCTGCTCGGCGGAAACAGCGTCACACTCGGTGCGGCTTTCGGCTGGCCAA-
GAACGGTTAACTTCGTGCCGC

M24-C:

CGCCGAGCAGCGAAGAATTGCAGGCGAACAAAGCGACCCTGGTGTGCCTGATTAGCGACT-
TTTATCCGGGAGCCGTGACA

FIG. 7I

M24-D:

TGTTTGGAGGGTGTGGTGGTCTCCACTCCCGCCTTGACGGGGCTGCTATCTGCCTTCCAG-
GCCACTGTCACGGCTCCCGG

M24-E:

CCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACGC-
CTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTG

M24-F:

GCATGCTTATCAGGCCTCAGTCGGCGCAACGGTTTTTTCCACGGTGCTCCCCTCATGCGT-
GACCTGGCAGCTGTAGCTTC

FIG. 7J

```
 M  K  Q  S  T  I  A  L  A  L  L  P  L  L  F  T  P
                                      SapI
                                     ~~~~~~~~
ATGAAACAAA GCACTATTGC ACTGGCACTC TTACCGTTGC TCTTCACCCC
TACTTTGTTT CGTGATAACG TGACCGTGAG AATGGCAACG AGAAGTGGGG

  V  T  K  A  D  Y  K  D  E  V  Q  L  V  E  S  G
                              MfeI
                             ~~~~~~
TGTTACCAAA GCCGACTACA AAGATGAAGT GCAATTGGTG GAAAGCGGCG
ACAATGGTTT CGGCTGATGT TTCTACTTCA CGTTAACCAC CTTTCGCCGC

G  G  L  V  Q  P  G  G  S  L  R  L  S  C  A  A  S
                                              BspEI
                                               ~~~
GCGGCCTGGT GCAACCGGGC GGCAGCCTGC GTCTGAGCTG CGCGGCCTCC
CGCCGGACCA CGTTGGCCCG CCGTCGGACG CAGACTCGAC GCGCCGGAGG

 G  F  T  F  S  S  Y  A  M  S  W  V  R  Q  A  P  G
BspEI                                      BstXI
~~~                                       ~~~~~~~~~~~~~
GGATTTACCT TTAGCAGCTA TGCGATGAGC TGGGTGCGCC AAGCCCCTGG

CCTAAATGGA AATCGTCGAT ACGCTACTCG ACCCACGCGG TTCGGGGACC
```

FIG. 8A

```
K  G  L   E  W  V  S   A  I  S   G  S  G   G  S  T
       XhoI
       ~~~~~~~
GAAGGGTCTC GAGTGGGTGA GCGCGATTAG CGGTAGCGGC GGCAGCACCT
CTTCCCAGAG CTCACCCACT CGCGCTAATC GCCATCGCCG CCGTCGTGGA

Y  Y  A  D   S  V  K   G  R  F  T   I  S  R   D  N  S
                                      PmlI      NspV
                                     ~~~~~~~    ~~~~
ATTATGCGGA TAGCGTGAAA GGCCGTTTTA CCATTTCACG TGATAATTCG
TAATACGCCT ATCGCACTTT CCGGCAAAAT GGTAAAGTGC ACTATTAAGC

 K  N  T  L   Y  L  Q   M  N  S   L  R  A  E   D  T  A
NspV                                                EagI
~~                                                  ~~~~
AAAAACACCC TGTATCTGCA AATGAACAGC CTGCGTGCGG AAGATACGGC
TTTTTGTGGG ACATAGACGT TTACTTGTCG GACGCACGCC TTCTATGCCG


  V  Y  Y   C  A  R  W   G  G  D   G  F  Y   A  M  D
EagI        BssHII
~~          ~~~~~~
CGTGTATTAT TGCGCGCGTT GGGGCGGCGA TGGCTTTTAT GCGATGGATT
```

FIG. 8B

```
GCACATAATAACGCGCGCAA CCCCGCCGCT ACCGAAAATA CGCTACCTAA
Y  W  G  Q   G  T  L   V  T  V  S   S  A  G   G  G  S
       StyI                        BlpI
      ~~~~~~~                     ~~~~~~~
ATTGGGGCCA AGGCACCCTG GTGACGGTTA GCTCAGCGGG TGGCGGTTCT
TAACCCCGGT TCCGTGGGAC CACTGCCAAT CGAGTCGCCC ACCGCCAAGA

 G  G  G  G   S  G  G   G  G  S   G  G  G  G   S  D  I
                                                  EcoRV
                                                  ~~~~~
GGCGGCGGTG GGAGCGGTGG CGGTGGTTCT GGCGGTGGTG GTTCCGATAT
CCGCCGCCAC CCTCGCCACC GCCACCAAGA CCGCCACCAC CAAGGCTATA

  V  M  T   Q  S  P  L   S  L  P   V  T  P   G  E  P
EcoRV        BanII
~            ~~~~~~
CGTGATGACC CAGAGCCCAC TGAGCCTGCC AGTGACTCCG GGCGAGCCTG
GCACTACTGG GTCTCGGGTG ACTCGGACGG TCACTGAGGC CCGCTCGGAC

A  S  I  S   C  R  S   S  Q  S  L   L  H  S   N  G  Y
            PstI
           ~~~~~~
CGAGCATTAG CTGCAGAAGC AGCCAAAGCC TGCTGCATAG CAACGGCTAT
GCTCGTAATC GACGTCTTCG TCGGTTTCGG ACGACGTATC GTTGCCGATA
```

FIG. 8C

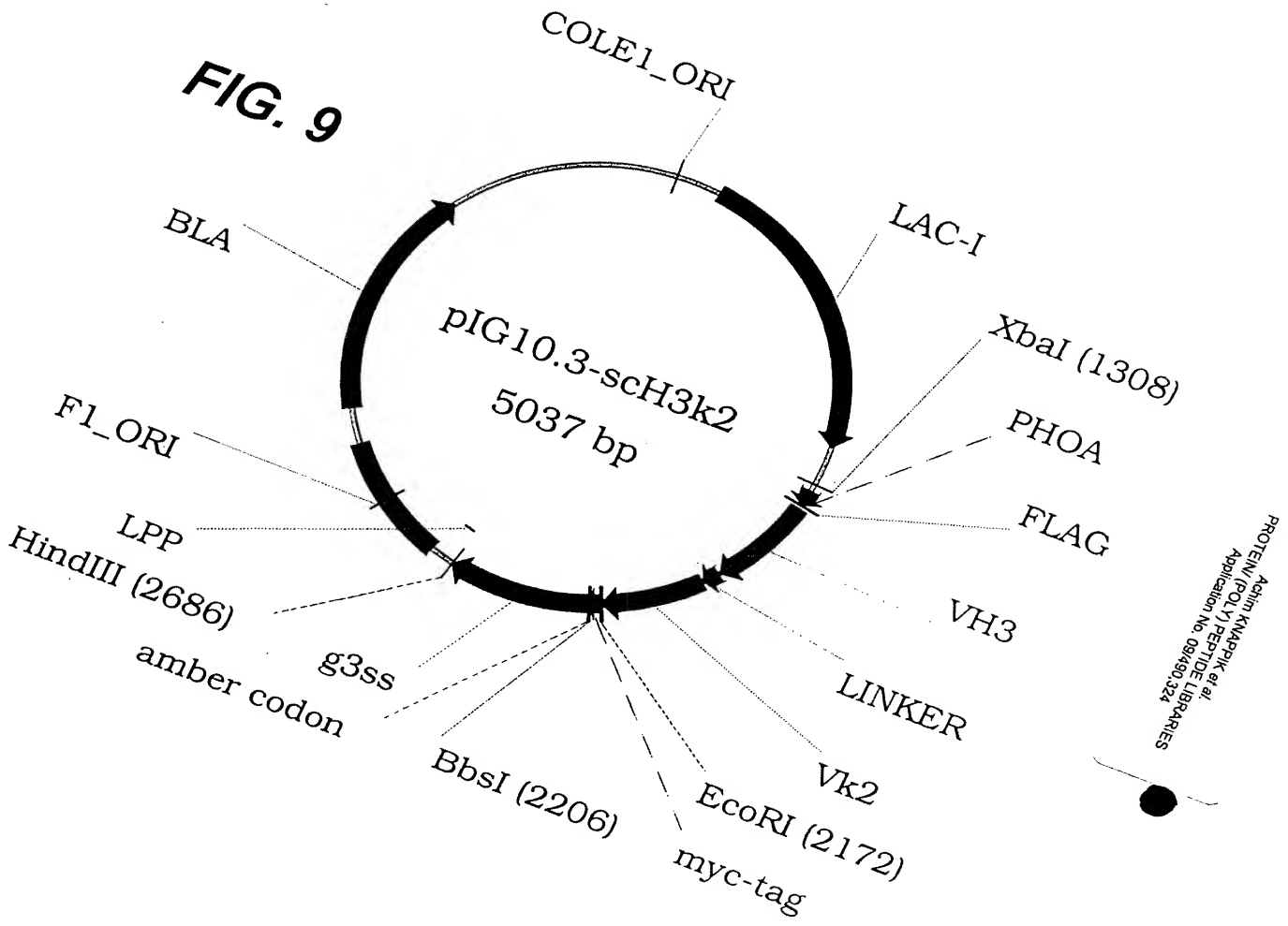
```
N  Y  L  D   W  Y  L   Q  K  P   G  Q  S  P   Q  L  L
              KpnI          SexAI                AseI
            ~~~~~~       ~~~~~~~~              ~~~
AACTATCTGG ATTGGTACCT TCAAAAACCA GGTCAAAGCC CGCAGCTATT
TTGATAGACC TAACCATGGA AGTTTTTGGT CCAGTTTCGG GCGTCGATAA

  I  Y  L   G  S  N  R   A  S  G   V  P  D   R  F  S
AseI                          Eco0109I
~~~                           ~~~~~~~~
AATTTATCTG GGCAGCAACC GTGCCAGTGG GGTCCCGGAT CGTTTTAGCG
TTAAATAGAC CCGTCGTTGG CACGGTCACC CCAGGGCCTA GCAAAATCGC

G  S  G  S   G  T  D   F  T  L  K   I  S  R   V  E  A
      BamHI
     ~~~~~~~
GCTCTGGATC CGGCACCGAT TTTACCCTGA AAATTAGCCG TGTGGAAGCT
CGAGACCTAG GCCGTGGCTA AAATGGGACT TTTAATCGGC ACACCTTCGA

 E  D  V  G   V  Y  Y   C  Q  Q   H  Y  T  T   P  P  T
 BbsI
~~~~~~
GAAGACGTGG GCGTGTATTA TTGCCAGCAG CATTATACCA CCCCGCCGAC
CTTCTGCACC CGCACATAAT AACGGTCGTC GTAATATGGT GGGGCGGCTG
```

FIG. 8D

```
F  G  Q   G  T  K  V   E  I  K   R  T  E   F
    MscI                          BsiWI EcoRI
   ~~~~~~                         ~~~~~~~~~~~
CTTTGGCCAG GGTACGAAAG TTGAAATTAA ACGTACGGAA TTC
GAAACCGGTC CCATGCTTTC AACTTTAATT TGCATGCCTT AAG
```

FIG. 8E

FIG. 9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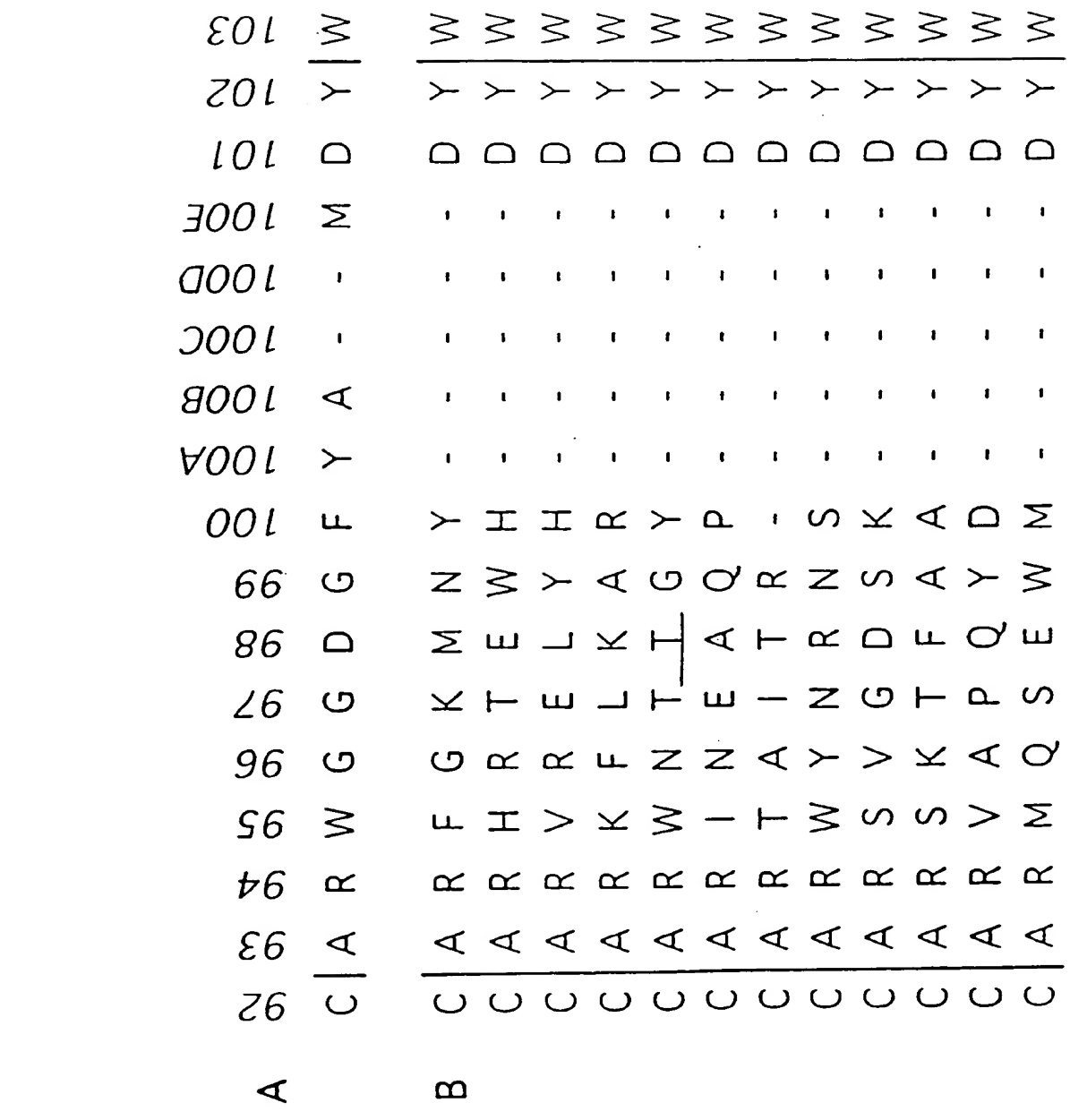
LAC-I
XbaI (1308)
PHOA
FLAG
VH3
LINKER
Vk2
EcoRI (2172)
myc-tag
BbsI (2206)
amber codon
g3ss
HindIII (2686)
LPP
F1_ORI
BLA
pIG10.3-scH3k2
5037 bp
PROTEIN/(POLY) PEPTIDE LIBRARIES
Application No. 09/496,324
Achim KWAPIK et al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C A R W G G D G F A
C A R W G G D G F A
C A R W G G D G F A
C A R W G G D G F A
C A R W G G D G F A
C A R W G G D G F A
C A R W G G D G F A
C A R W G G D G F A
C A R W G G D G F A
C A R W G G D G F A
C A R W G G D G F A
C A R W G G D G F A
C A R W G G D G F A
A
B

FIG. 10A

C	C	A	R	Y	F	V	H	F	L	Y	T	M	V	M	D	V	W
	C	A	R	M	A	L	R	A	S	G	K	Y	I	M	D	V	W
	C	A	R	K	N	Q	M	V	F	H	A	R	K	F	D	V	W
	C	A	R	T	Q	S	F	W	E	Q	Q	K	V	M	D	Y	W
	C	A	R	Y	P	Y	R	S	N	F	F	M	P	M	D	V	W
	C	A	R	*	G	S	G	S	E	H	W	S	I	F	D	V	W
	C	A	R	R	N	P	W	N	V	N	Y	L	H	F	D	V	W
	C	A	R	M	K	P	M	L	N	R	D	G	T	M	D	V	W
	C	A	R	K	G	S	E	F	L	E	T	D	V	M	D	Y	W
	C	A	R	S	W	T	N	D	K	P	N	F	I	M	D	V	W
	C	A	R	Y	A	G	T	T	F	K	Q	G	P	M	D	Y	W

FIG. 10B

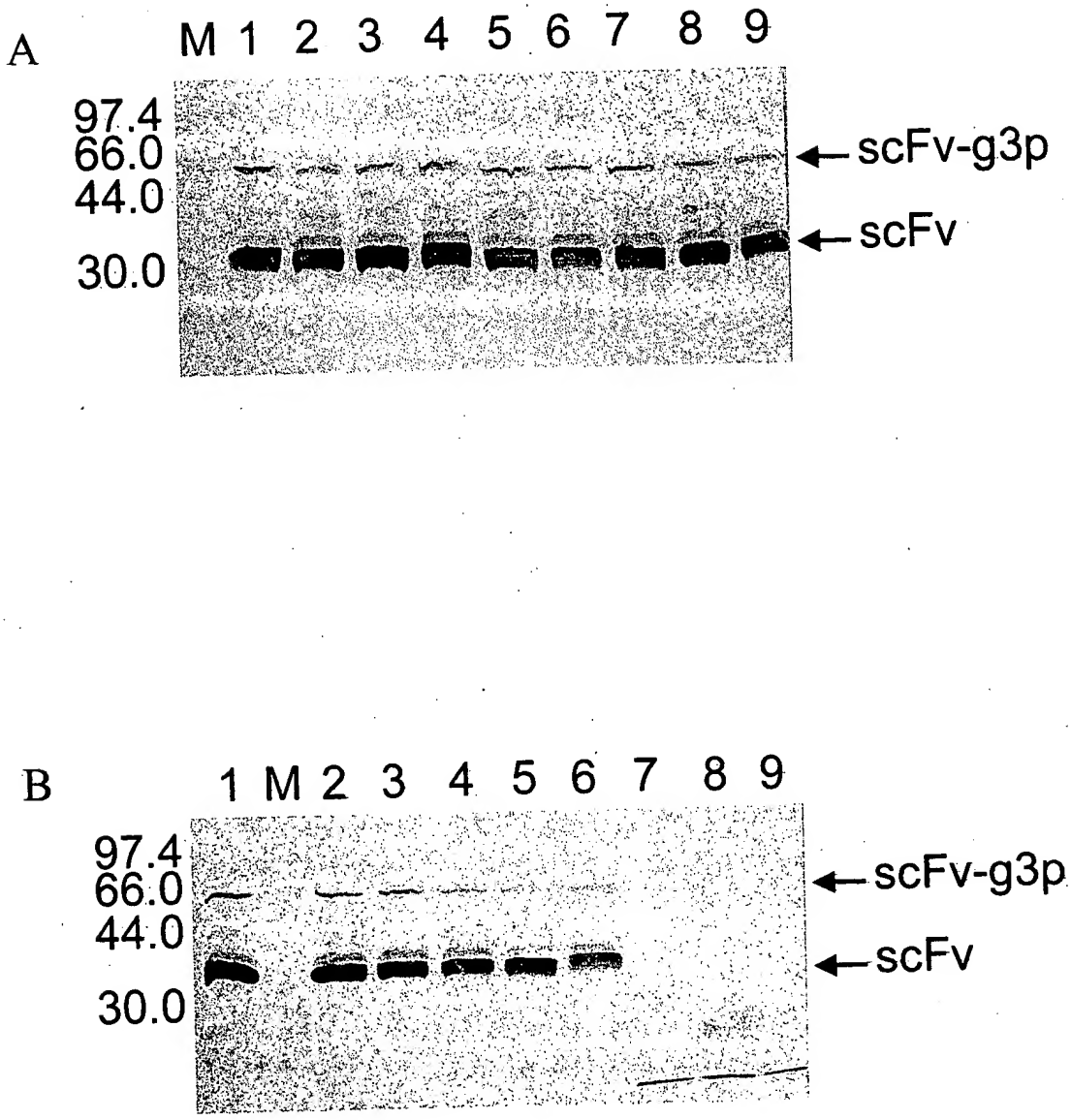

A
M 1 2 3 4 5 6 7 8 9
97.4
66.0
44.0
30.0
scFv-g3p
scFv
B
1 M 2 3 4 5 6 7 8 9
97.4
66.0
44.0
30.0
scFv-g3p
scFv

FIG. 11

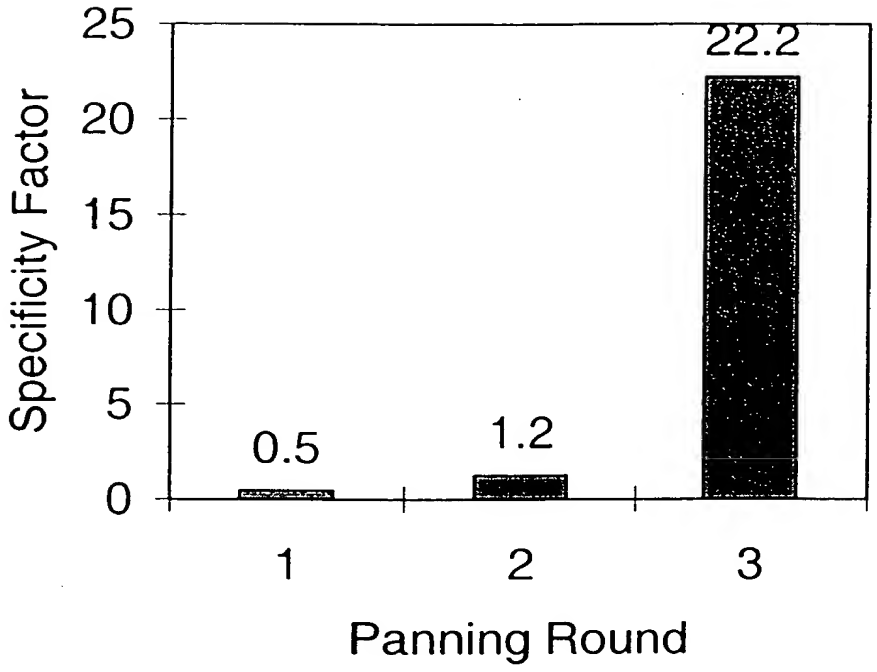


FIG. 12

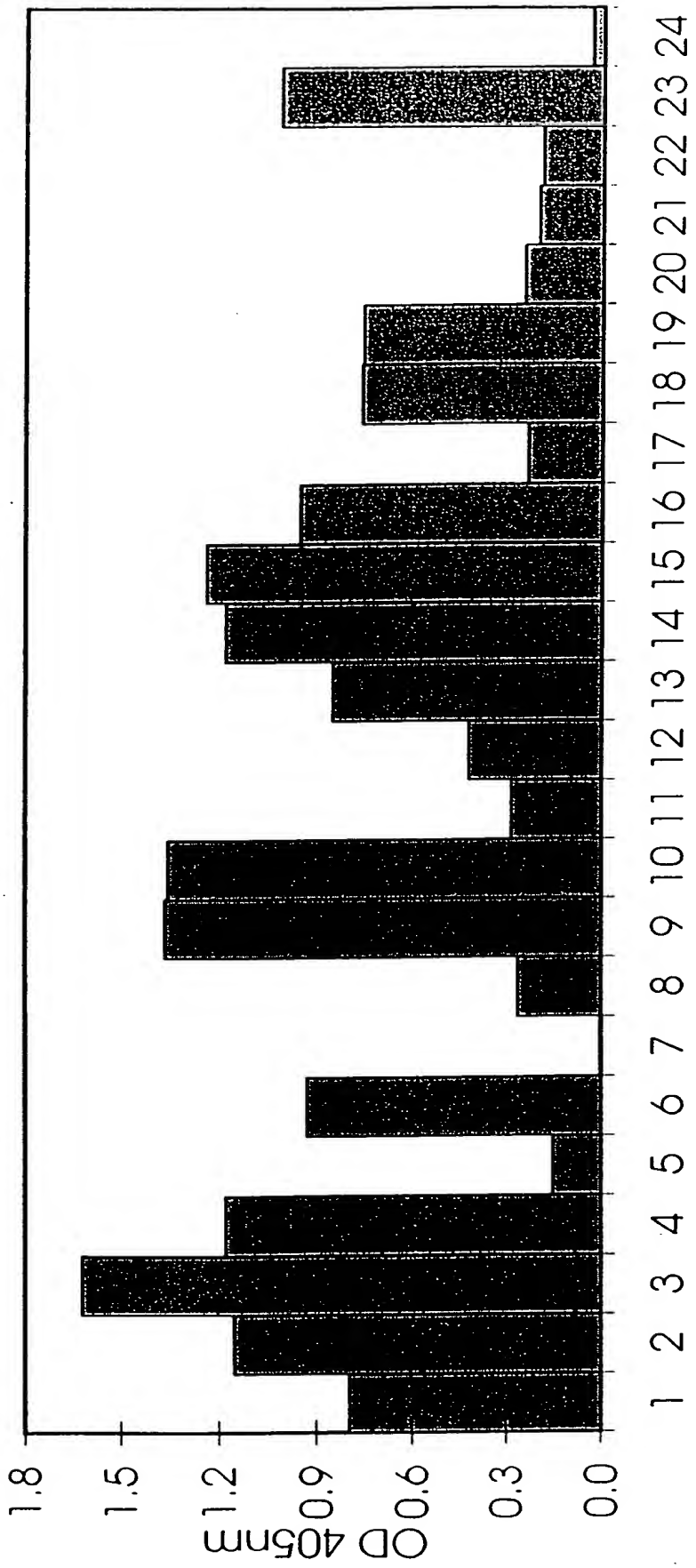

OD 405nm
1.8
1.5
1.2
0.9
0.6
0.3
0.0
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24
Clone Number

FIG. 13

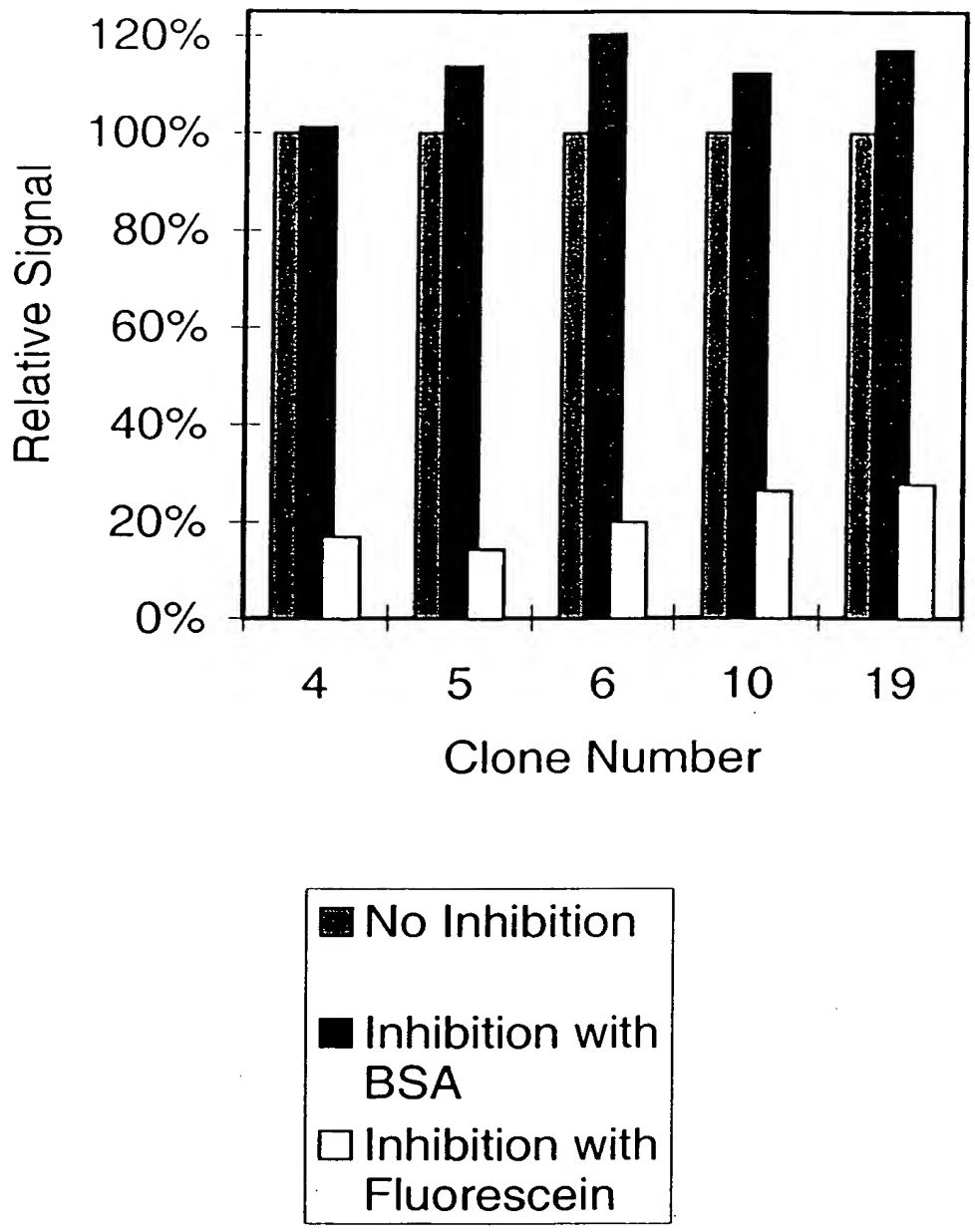

120%
100%
80%
60%
40%
20%
0%
Relative Signal
4
5
6
10
19
Clone Number
No Inhibition
Inhibition with BSA
Inhibition with Fluorescein

FIG. 14

92	*93*	*94*	*95*	*96*	*97*	*98*	*99*	*100*	*100A*	*100B*	*100C*	*100D*	*100E*	*101*	*102*	*103*	*Frequency*
C	A	R	K	R	M	M	Q	N	P	R	F	R	F	D	V	W	1
C	A	R	R	S	K	Q	K	R	K	M	R	R	F	D	V	W	3
C	A	R	R	N	G	K	R	H	L	R	H	R	F	D	V	W	1
C	A	R	R	K	M	R	K	R	I	K	R	R	F	D	V	W	2
C	A	R	Y	R	K	I	M	K	W	K	N	S	F	D	V	W	1
C	A	R	L	I	E	V	H	P	S	F	D	Q	M	D	V	W	1
C	A	R	R	K	P	M	F	L	K	K	A	V	F	D	V	W	1
C	A	R	R	K	F	H	R	Y	S	T	V	K	F	D	Y	W	2
C	A	R	R	K	T	M	R	S	R	V	K	Y	F	D	Y	W	1
C	A	R	K	K	R	S	W	R	R	M	D	R	F	D	V	W	1
C	A	R	R	N	P	R	R	G	R	M	N	R	F	D	V	W	1
C	A	R	K	G	K	K	K	F	A	R	P	R	F	D	V	W	1
C	A	R	R	M	V	H	K	G	K	R	K	I	F	D	V	W	1
C	A	R	R	K	H	I	T	Y	P	R	K	Q	F	D	V	W	1
C	A	R	R	W	T	K	R	R	S	F	A	R	F	D	V	W	1
C	A	R	K	K	L	K	Q	Y	T	F	S	R	F	D	Y	W	1

FIG. 15

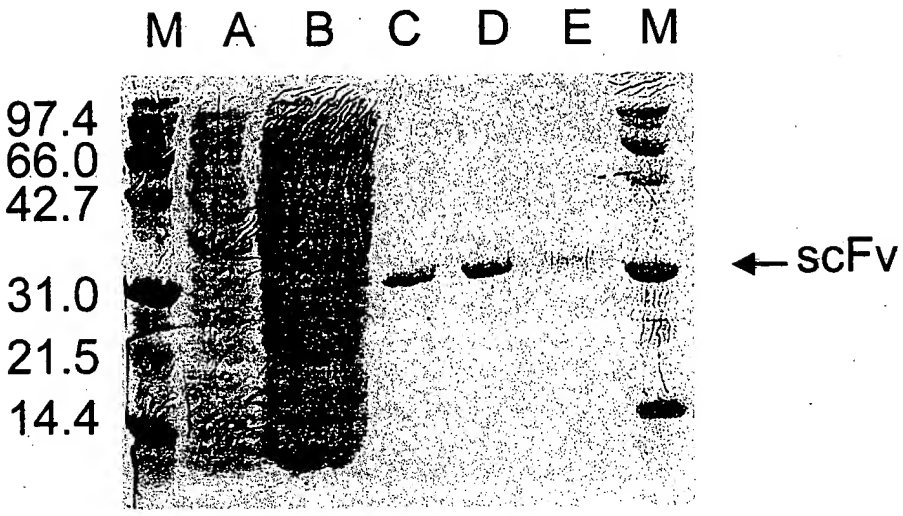


FIG. 16

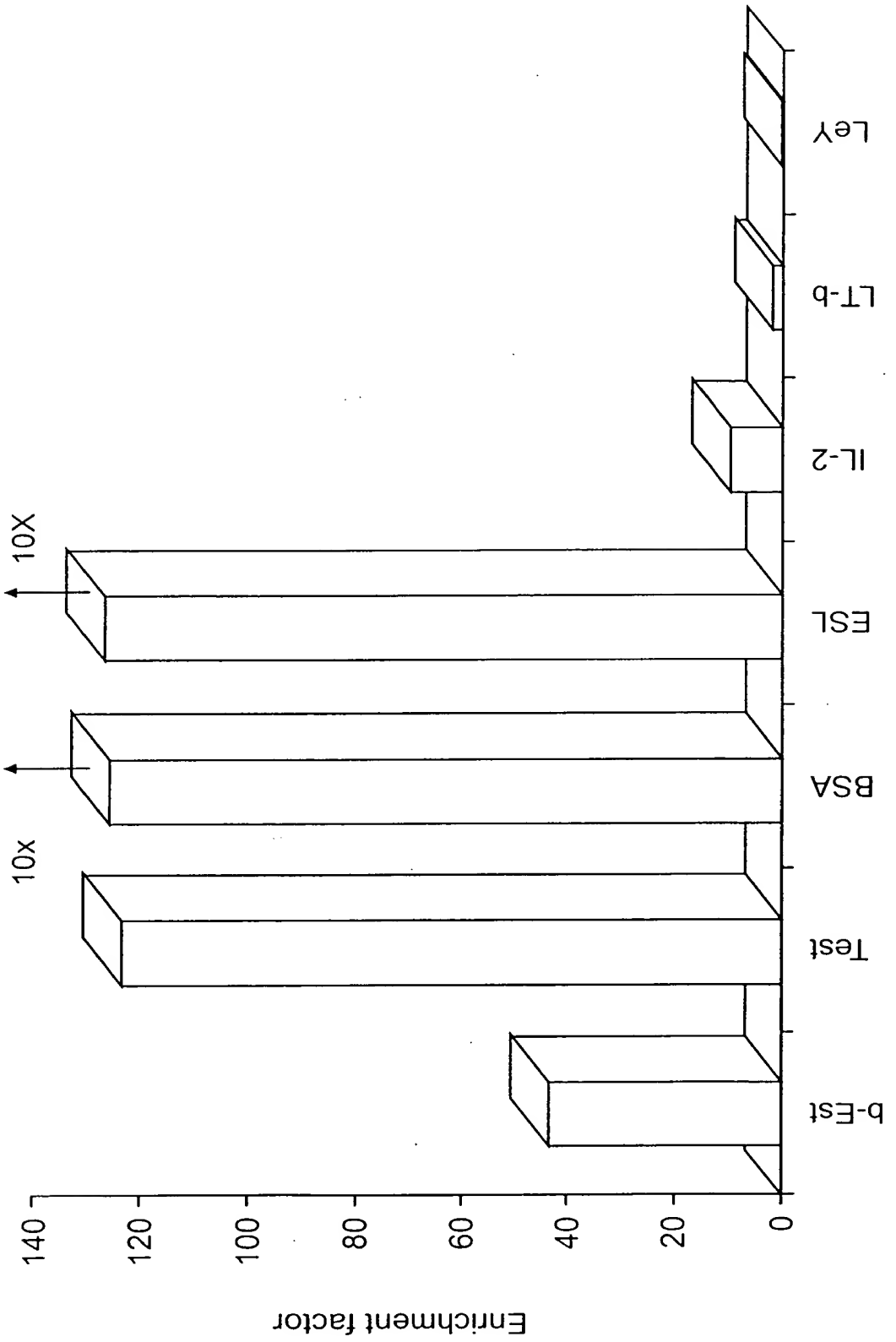

Enrichment factor
0
20
40
60
80
100
120
140
b-Est
Test
BSA
ESL
IL-2
LT-b
LeY
Antigen
10x
10X

FIG. 17

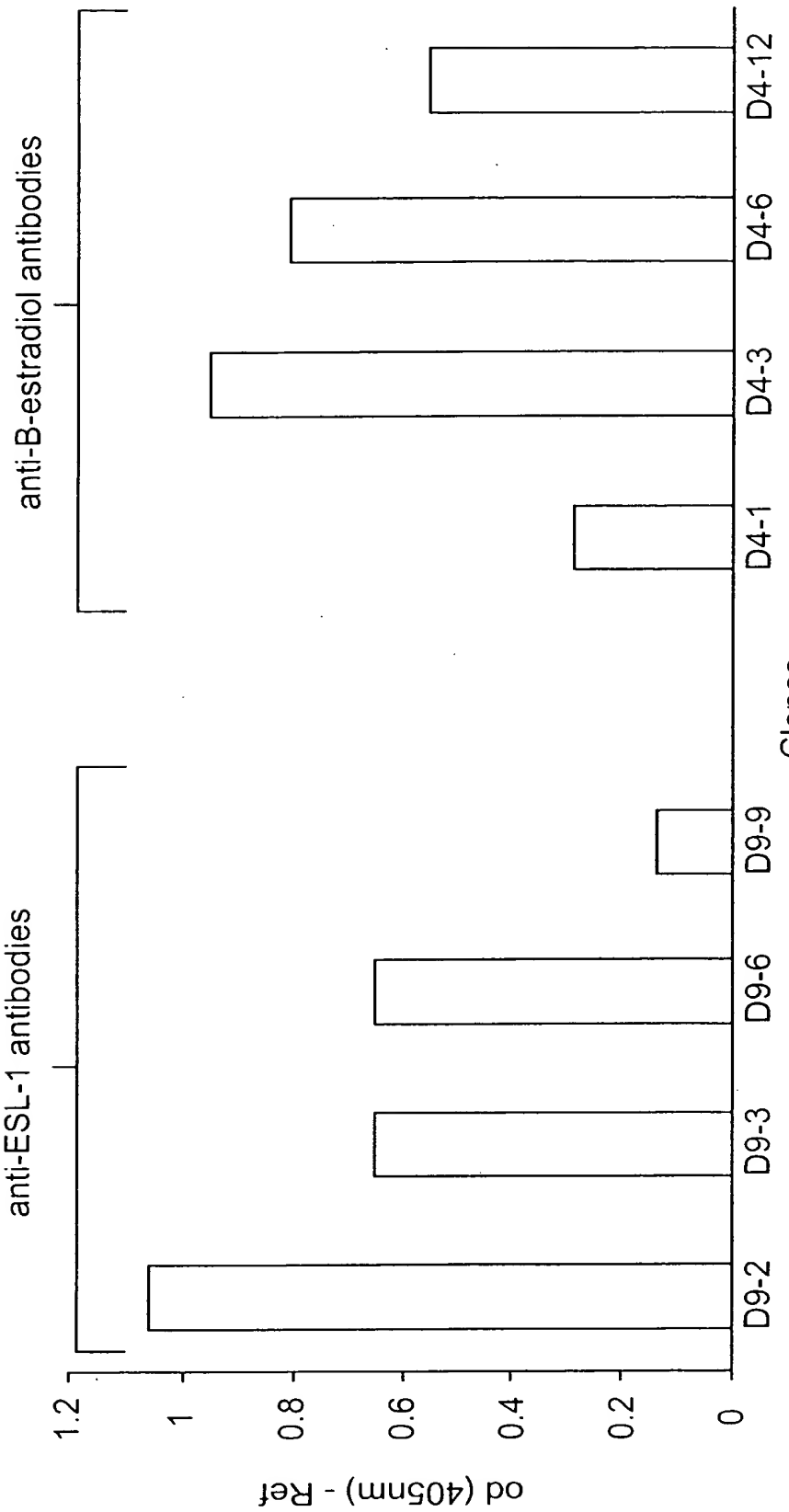

od (405nm) - Ref
1.2
1
0.8
0.6
0.4
0.2
0
D9-2
D9-3
D9-6
D9-9
D4-1
D4-3
D4-6
D4-12
Clones
anti-ESL-1 antibodies
anti-B-estradiol antibodies

FIG. 18

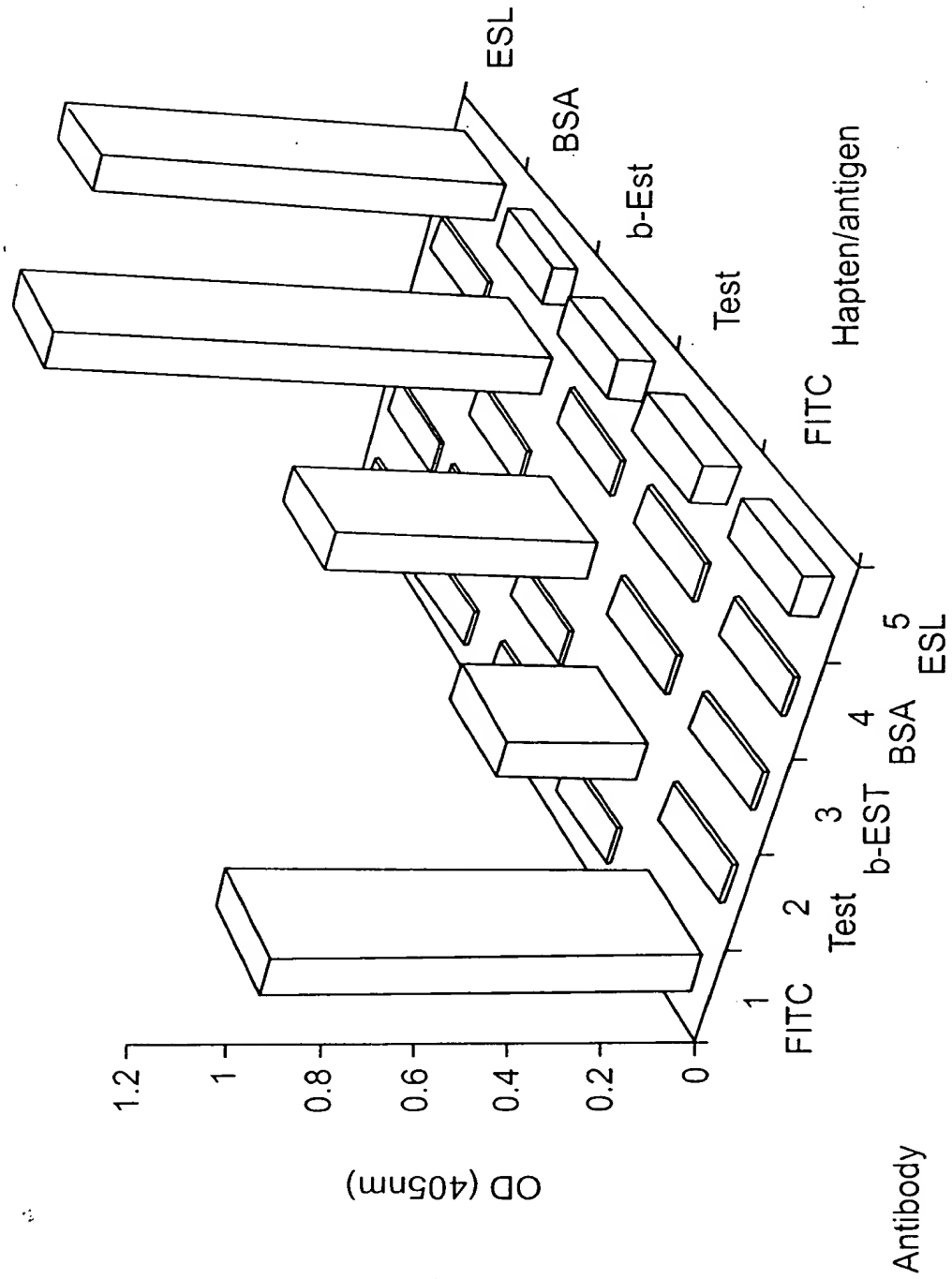

OD (405nm)
1.2
1
0.8
0.6
0.4
0.2
0
Antibody
1
FITC
2
Test
3
b-EST
4
BSA
5
ESL
Hapten/antigen
FITC
Test
b-Est
BSA
ESL

FIG. 19

92	93	94	95	96	97	98	99	100	100A	100B	100C	100D	100E	101	102	103	FREQUENCY
C	A	R	T	R	P	W	Q	A	T	R	K	G	F	D	V	W	3
C	A	R	N	Q	W	E	F	K	N	R	R	K	M	D	Y	W	8
C	A	R	K	R	W	M	W	P	I	G	K	R	F	D	Y	W	7
C	A	R	Y	S	L	W	R	L	D	E	Y	F	F	D	Y	W	1
C	A	R	V	P	W	G	D	F	W	S	W	H	M	D	V	W	1
C	A	R	N	G	L	E	P	R	H	R	K	M	M	D	Y	W	1
C	A	R	I	M	K	A	P	P	-	-	-	-	-	D	Y	W	1
C	A	R	R	K	T	W	H	W	F	Y	K	R	M	D	Y	W	1
C	A	R	W	K	D	M	W	S	Q	V	Y	V	M	D	Y	W	1
C	A	R	N	K	Q	Q	M	R	F	R	R	F	M	D	Y	W	5
C	A	R	N	M	L	A	L	S	R	G	K	E	M	D	V	W	4
C	A	R	N	M	R	L	M	R	M	R	K	N	F	D	V	W	1

FIG. 20

92	93	94	95	96	97	98	99	100	100A	100B	100C	100D	100E	101	102	103	FREQUENCY
C	A	R	Y	I	K	Q	A	K	R	K	L	A	F	D	Y	W	4
C	A	R	Y	N	R	H	A	W	Q	K	M	Q	F	D	Y	W	3
C	A	R	Y	V	K	Y	A	R	N	K	M	Q	F	D	Y	W	2
C	A	R	Y	K	R	G	A	W	M	K	T	M	F	D	V	W	1
C	A	R	R	K	P	L	R	R	I	M	K	W	F	D	Y	W	1
C	A	R	Y	R	K	R	A	S	R	Q	M	Q	F	D	Y	W	1

FIG. 21

92	93	94	95	96	97	98	99	100	100A	100B	100C	100D	100E	101	102	103	FREQUENCY
C	A	R	Q	R	Y	R	S	K	I	K	G	H	F	D	V	W	16
C	A	R	_	W	R	D	F	N	S	Y	D	P	M	D	Y	W	1
C	A	R	M	A	D	L	D	N	Y	W	V	Q	F	D	Y	W	1
C	A	R	L	Q	A	Y	L	K	P	H	H	W	M	D	Y	W	1
C	A	R	R	L	I	E	Q	A	R	D	H	V	M	D	Y	W	1
C	A	R	S	W	H	N	S	Q	F	T	Q	S	F	D	V	W	1
C	A	R	V	D	H	F	Q	T	E	N	E	W	M	D	Y	W	1
C	A	R	D	W	P	T	L	I	F	W	Y	W	F	D	Y	W	1

FIG. 22

92	93	94	95	96	97	98	99	100	100A	100B	100C	100Ca	100D	100E	101	102	103	FREQUENCY
C	A	R	G	F	G	F	T	E	-	-	-	-	-	-	D	Y	W	4
C	A	R	Q	F	D	E	D	S	F	V	R	-	R	F	D	V	W	4
C	A	R	I	L	K	E	S	S	K	S	R	-	Q	M	D	V	W	2
C	A	R	E	Q	D	E	Y	G	A	I	R	-	I	M	D	Y	W	1
C	A	R	N	H	F	E	A	S	W	P	R	R	Q	M	D	V	W	1
C	A	R	E	N	E	W	V	D	M	I	L	-	D	M	D	Y	W	2
C	A	R	Q	Y	S	E	T	R	W	V	R	-	K	F	D	Y	W	1
C	A	R	Q	F	K	E	S	K	T	R	R	-	K	F	D	V	W	13
C	A	R	K	K	T	Q	Y	V	H	D	W	-	R	M	D	V	W	3
C	A	R	R	W	R	E	T	K	S	K	R	-	F	F	D	V	W	1
C	A	R	D	Y	I	M	E	F	-	-	-	-	-	-	D	Y	W	1
C	A	R	Q	F	E	E	T	K	Q	R	R	-	L	M	D	Y	W	1

FIG. 23

92	93	94	95	96	97	98	99	100	100A	100B	100C	100D	100E	101	102	103	FREQUENCY
C	A	R	D	Q	G	F	Y	A	I	D	Y	V	M	D	Y	W	5
C	A	R	V	F	T	Y	M	Y	N	Y	F	R	F	D	V	W	1
C	A	R	V	F	F	E	Q	M	E	V	V	R	M	D	V	W	1
C	A	R	E	K	E	Y	R	L	S	W	S	Q	M	D	Y	W	1
C	A	R	Y	P	S	R	W	A	P	N	W	Y	M	D	Y	W	1
C	A	R	D	G	G	F	K	P	L	T	H	F	F	D	V	W	1

FIG. 24

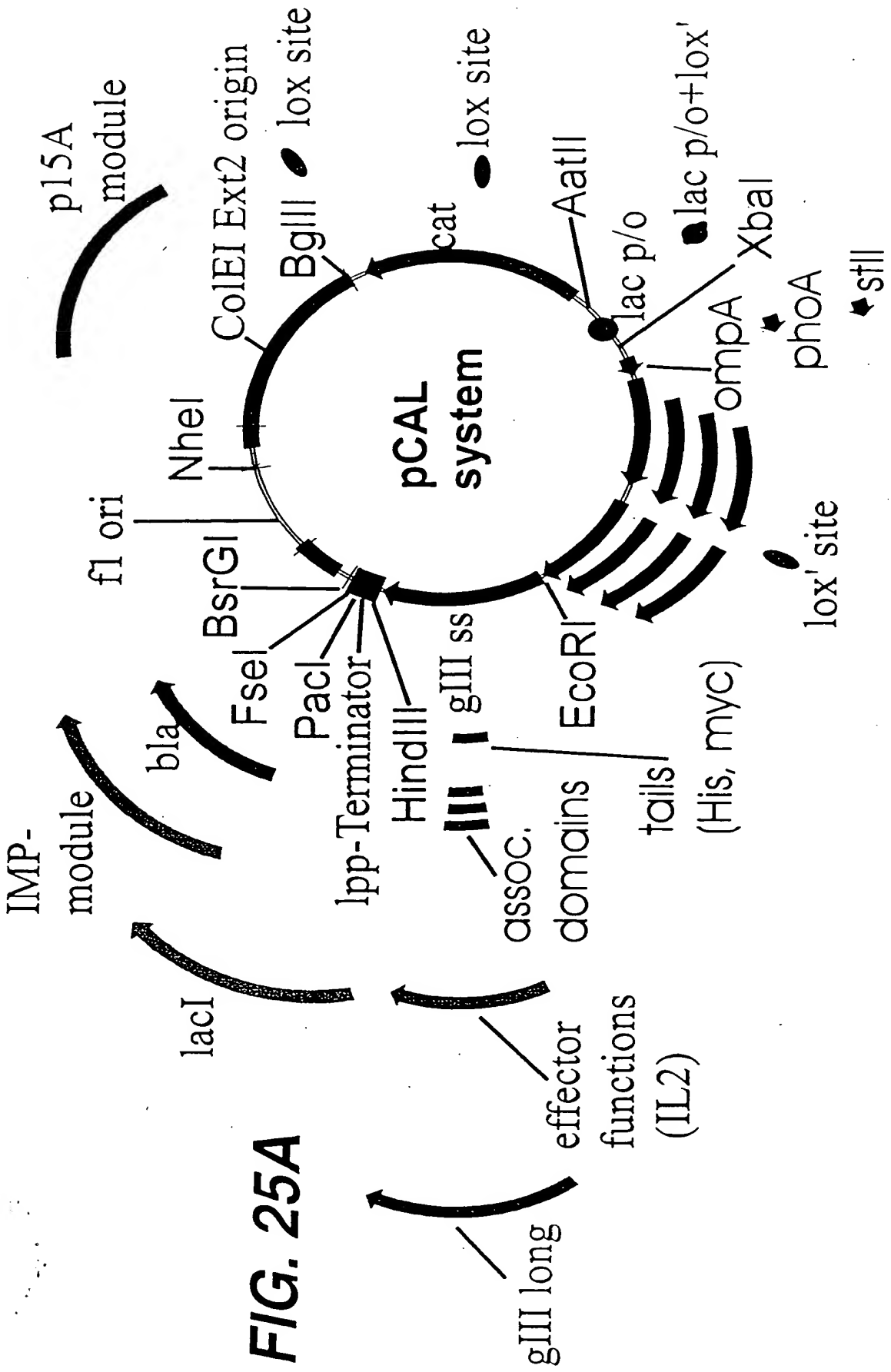

p15A module
ColEI Ext2 origin
BglII
lox site
cat
lox site
AatII
lac p/o
lac p/o+lox'
XbaI
ompA
phoA
stII
lox' site
pCAL system
f1 ori
NheI
BsrGI
FseI
PacI
lpp-Terminator
HindIII
gIII ss
EcoRI
tails (His, myc)
assoc. domains
effector functions (IL2)
gIII long
lacI
IMP-module
bla

FIG. 25A

unique restriction site	Isoschizomers
AatII	/
AflII	BfrI, BspTI, Bst98I
AscI	/
AseI	VspI, AsnI, PshBI
BamHI	BstI
BbeI	EheI, KasI, NarI
BbsI	BpuAI, BpiI
BglII	/
BlpI	Bpu1102I,CelII, BlpI
BsaBI	MamI, Bsh1365I, BsrBRI
BsiWI	Pfl23II, SpII, SunI
BspEI	AccIII, BseAI, BsiMI, Kpn2I, MroI
BsrGI	Bsp1407I, SspBI
BssHII	PauI
BstEII	BstPI, Eco91I, EcoO651
BstXI	/
Bsu36I	AocI, CvnI, Eco81I
DraIII	/
DsmAI	
EagI	BstZI, EclXI, Eco52I, XmaIII
Eco57I	/
EcoO109I	DraII
EcoRI	/
EcoRV	Eco32I
FseI	/
HindIII	/
HpaI	/
KpnI	Acc65I, Asp718I
MluI	/
MscI	BaII, MluNI

FIG. 25B

unique restriction site	Isoschizomers
MunI	MfeI
NheI	/
NsiI	Ppu10I, EcoT22I, Mph1103I
NspV	Bsp119I, BstBI, Csp45I, LspI, SfuI
PacI	/
PmeI	/
PmlI	BbrPI, Eco72I, PmaCI
Psp5II	PpuMI
PstI	/
RsrII	(RsriI), CpoI, CspI
SanDI	/
SapI	/
SexAI	/
SpeI	/
SfiI	/
SphI	BbuI, PaeI,NspI
StuI	AatI, Eco147I
StyI	Eco130I, EcoT14I
XbaI	BspLU11II
XhoI	PaeR7I
XmaI	AvaI, SmaI, Cfr9I, PspAI

FIG. 25C

No	module/flanking restriction sites	functional element	sites to be removed	sites to be inserted	template	reference
M1	AatII-lacp/o-XbaI	lac promotor/operator	2x VspI (AseI)	AatII	vector pASK30	Skerra et al. (1991) Bio/Technology 9, 273-278
M2	BglII-lox-AatII	Cre/lox recombination site	2x VspI (AseI)	lox, BglII	(synthetic)	Hoess et al. (1986) Nucleic Acids Res. 2287-2300
M3	XbaI-lox'-SphI	Cre/lox' recombination site	none	lox', SphI	(synthetic)	see M2
M7-I	EcoRI-gIIIlong-HindIII	gIIIp of filamentous phage with N-terminal myctail/amber codon	SphI, BamHI	none	vector pIG10	Ge et al., (1994) Expressing antibodies in E. coli. In: Antibody engineering: A practical approach. IRL Press, New York, pp 229-266

FIG. 26A

M7-II	EcoRI-gIIIss-HindIII	truncated gIIIp of filamentous phage with N-terminal Gly-Ser linker	SphI		vector pIG10	see M7-I
M7-III	EcoRI-gIIIss-HindIII	truncated gIIIp of filamentous phage with N-terminal myctail/amber codon	SphI, BbsI		vector pIG10	see M7-I
M8	SphI-lox-HindIII	Cre/lox recombination site	none	lox	(synthetic)	see M3
M9-II	HindIII-lpp-PacI	lpp-terminator	none	PacI, FseI	(synthetic)	see M1
M10-II	PacI/FseI-bla-BsrGI	beta-lactamase/bla (ampR)	VspI, Eco57I, BssSI	PacI, FseI, BsrGI	pASK30	see M1
M11-II	BsrGI-f1 ori-NheI	origin of single-stranded replication	DraIII (BanII not removed)	BsrGI, NheI	pASK30	see M1
M11-III	BsrGI-f1 ori-NheI	origin of single-stranded replication	DraIII, BanII	BsrGI, NheI	pASK30	see M1

FIG. 26B

M12	NheI-p15A-BglII	origin of double-stranded replication	BssSI, VspI, NspV	NheI, BglII	pACYC184	Rose, R.E. (1988) Nucleic Acids Res. 16, 355
M13	BglII-lox-BglII	Cre/lox recombination site	none	BglII, lox, XmnI	(synthetic)	see M3
M14-Ext2	BglII-ColEI-NheI	origin of double-stranded replication	Eco57I (BssSI not removed)	BglII, NheI	pUC19	Yanisch-Peron, C. (1985) Gene 33,103-119
M17	AatII-cat-BglII	chloramphenicol-acetyltransferase/ cat (camR)	BspEI, MscI, StyI/NcoI		pACYC184	Cardoso, M. & Schwarz,S. (1992) J. Appl. Bacteriol.72, 289-293
M19	XbaI-phoA-EcoRI	signal sequence of phosphatase A	(synthetic)		(synthetic)	see M1
M20	XbaI-phoA-FLAG-EcoRI	signal sequence of phosphatase A + FLAG detection tag	(synthetic)		(synthetic)	Knappik, A & Plückthun, A. (1994) BioTechniques 17, 754-761

FIG. 26C

M21	XbaI-stII-SapI	heat-stable enterotoxin II signal sequence	(synthetic)		(synthetic)	Lee et al. (1983) Infect. Immunol. 264-268
M41	AflII-lacI-NheI	lac-repressor	BstXI, MluI,BbsI, BanII, BstEII, HpaI, BbeI, VspI		pASK30	see M1
M42	EcoRI-Histail-HindIII	poly-histidine tail	(synthetic)		(synthetic)	Lindner et al., (1992) Methods: a companion to methods in enzymology 4, 41-56

FIG. 26D

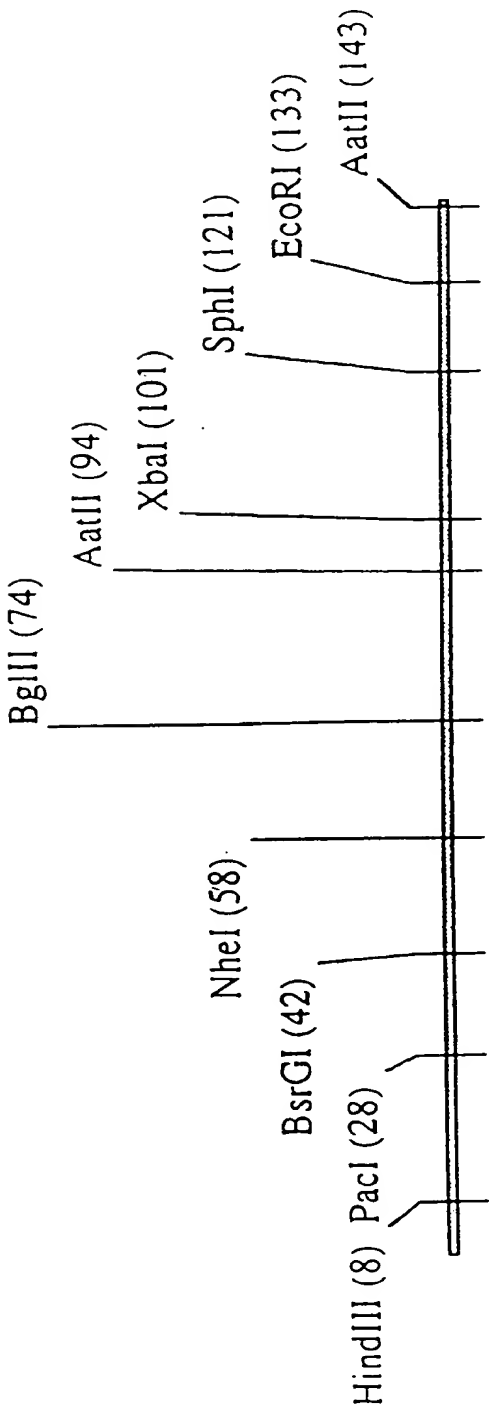

BglII (74)
AatII (94)
XbaI (101)
SphI (121)
EcoRI (133)
AatII (143)
NheI (58)
BsrGI (42)
HindIII (8)
PacI (28)
MCS
143 bp

FIG. 27A

```
          HindIII                PacI                  BsrGI
          ~~~~~~~              ~~~~~~~~              ~~~~~~
  1   ACATGTAAGC TTCCCCCCCC CCTTAATTAA CCCCCCCCCC TGTACACCCC
      TGTACATTCG AAGGGGGGGG GGAATTAATT GGGGGGGGGG ACATGTGGGG

           NheI                BglII                AatII   XbaI
          ~~~~~~~              ~~~~~~              ~~~~~~~    ~
  51  CCCCCCGCTA GCCCCCCCCC CCAGATCTCC CCCCCCCCGA CGTCCCCCCT
      GGGGGGCGAT CGGGGGGGGG GGTCTAGAGG GGGGGGGGCT GCAGGGGGGA

      XbaI                 SphI                 EcoRI AatII
      ~~~~~              ~~~~~~~              ~~~~~~~~~~~
 101  CTAGACCCCC CCCCCGCATG CCCCCCCCCC CGAATTCGAC GTC
      GATCTGGGGG GGGGGCGTAC GGGGGGGGGG GCTTAAGCTG CAG
```

FIG. 27B

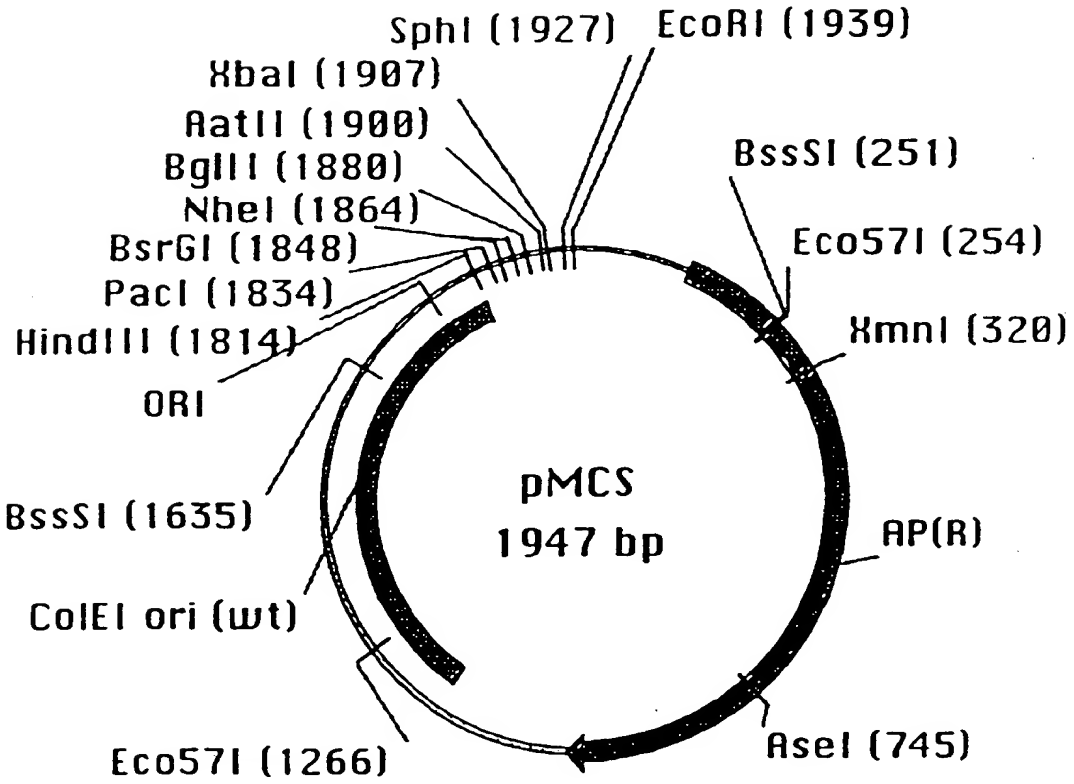

SphI (1927)
EcoRI (1939)
XbaI (1907)
AatII (1900)
BglII (1880)
NheI (1864)
BsrGI (1848)
PacI (1834)
HindIII (1814)
ORI
BssSI (1635)
ColEI ori (wt)
Eco57I (1266)
BssSI (251)
Eco57I (254)
XmnI (320)
pMCS
1947 bp
AP(R)
AseI (745)

FIG. 28A

```
  1  CAGGTGGCAC TTTTCGGGGA AATGTGCGCG GAACCCCTAT TTGTTTATTT
     GTCCACCGTG AAAAGCCCCT TTACACGCGC CTTGGGGATA AACAAATAAA

 51  TTCTAAATAC ATTCAAATAT GTATCCGCTC ATGAGACAAT AACCCTGATA
     AAGATTTATG TAAGTTTATA CATAGGCGAG TACTCTGTTA TTGGGACTAT

101  AATGCTTCAA TAATATTGAA AAAGGAAGAG TATGAGTATT CAACATTTCC
     TTACGAAGTT ATTATAACTT TTTCCTTCTC ATACTCATAA GTTGTAAAGG

151  GTGTCGCCCT TATTCCCTTT TTTGCGGCAT TTTGCCTTCC TGTTTTTGCT
     CACAGCGGGA ATAAGGGAAA AAACGCCGTA AAACGGAAGG ACAAAAACGA

                                      Eco57I
                                      ~~~~~~
201  CACCCAGAAA CGCTGGTGAA AGTAAAAGAT GCTGAAGATC AGTTGGGTGC
     GTGGGTCTTT GCGACCACTT TCATTTTCTA CGACTTCTAG TCAACCCACG
                                                  BssSI
                                                  ~

251  ACGAGTGGGT TACATCGAAC TGGATCTCAA CAGCGGTAAG ATCCTTGAGA
     TGCTCACCCA ATGTAGCTTG ACCTAGAGTT GTCGCCATTC TAGGAACTCT
    BssSI
    ~~~~~
```

FIG. 28B

Xmn I

```
301  GTTTTCGCCC CGAAGAACGT TTTCCAATGA TGAGCACTTT TAAAGTTCTG
     CAAAAGCGGG GCTTCTTGCA AAAGGTTACT ACTCGTGAAA ATTTCAAGAC

351  CTATGTGGCG CGGTATTATC CCGTATTGAC GCCGGGCAAG AGCAACTCGG
     GATACACCGC GCCATAATAG GGCATAACTG CGGCCCGTTC TCGTTGAGCC

401  TCGCCGCATA CACTATTCTC AGAATGACTT GGTTGAGTAC TCACCAGTCA
     AGCGGCGTAT GTGATAAGAG TCTTACTGAA CCAACTCATG AGTGGTCAGT

451  CAGAAAAGCA TCTTACGGAT GGCATGACAG TAAGAGAATT ATGCAGTGCT
     GTCTTTTCGT AGAATGCCTA CCGTACTGTC ATTCTCTTAA TACGTCACGA

501  GCCATAACCA TGAGTGATAA CACTGCGGCC AACTTACTTC TGACAACGAT
     CGGTATTGGT ACTCACTATT GTGACGCCGG TTGAATGAAG ACTGTTGCTA

551  CGGAGGACCG AAGGAGCTAA CCGCTTTTTT GCACAACATG GGGGATCATG
     GCCTCCTGGC TTCCTCGATT GGCGAAAAAA CGTGTTGTAC CCCCTAGTAC

601  TAACTCGCCT TGATCGTTGG GAACCGGAGC TGAATGAAGC CATACCAAAC
     ATTGAGCGGA ACTAGCAACC CTTGGCCTCG ACTTACTTCG GTATGGTTTG

651  GACGAGCGTG ACACCACGAT GCCTGTAGCA ATGGCAACAA CGTTGCGCAA
```

FIG. 28C

```
      CTGCTCGCAC TGTGGTGCTA CGGACATCGT TACCGTTGTT GCAACGCGTT

                                                      AseI
                                                     ~~~~~~
 701  ACTATTAACT GGCGAACTAC TTACTCTAGC TTCCCGGCAA CAATTAATAG
      TGATAATTGA CCGCTTGATG AATGAGATCG AAGGGCCGTT GTTAATTATC

 751  ACTGGATGGA GGCGGATAAA GTTGCAGGAC CACTTCTGCG CTCGGCCCTT
      TGACCTACCT CCGCCTATTT CAACGTCCTG GTGAAGACGC GAGCCGGGAA

 801  CCGGCTGGCT GGTTTATTGC TGATAAATCT GGAGCCGGTG AGCGTGGGTC
      GGCCGACCGA CCAAATAACG ACTATTTAGA CCTCGGCCAC TCGCACCCAG

 851  TCGCGGTATC ATTGCAGCAC TGGGGCCAGA TGGTAAGCCC TCCCGTATCG
      AGCGCCATAG TAACGTCGTG ACCCCGGTCT ACCATTCGGG AGGGCATAGC

 901  TAGTTATCTA CACGACGGGG AGTCAGGCAA CTATGGATGA ACGAAATAGA
      ATCAATAGAT GTGCTGCCCC TCAGTCCGTT GATACCTACT TGCTTTATCT

 951  CAGATCGCTG AGATAGGTGC CTCACTGATT AAGCATTGGT AACTGTCAGA
      GTCTAGCGAC TCTATCCACG GAGTGACTAA TTCGTAACCA TTGACAGTCT

1001  CCAAGTTTAC TCATATATAC TTTAGATTGA TTTAAAACTT CATTTTTAAT
      GGTTCAAATG AGTATATATG AAATCTAACT AAATTTTGAA GTAAAAATTA
```

FIG. 28D

```
1051   TTAAAAGGAT CTAGGTGAAG ATCCTTTTTG ATAATCTCAT GACCAAAATC
       AATTTTCCTA GATCCACTTC TAGGAAAAAC TATTAGAGTA CTGGTTTTAG

1101   CCTTAACGTG AGTTTTCGTT CCACTGAGCG TCAGACCCCG TAGAAAAGAT
       GGAATTGCAC TCAAAAGCAA GGTGACTCGC AGTCTGGGGC ATCTTTTCTA

1151   CAAAGGATCT TCTTGAGATC CTTTTTTTCT GCGCGTAATC TGCTGCTTGC
       GTTTCCTAGA AGAACTCTAG GAAAAAAAGA CGCGCATTAG ACGACGAACG

1201   AAACAAAAAA ACCACCGCTA CCAGCGGTGG TTTGTTTGCC GGATCAAGAG
       TTTGTTTTTT TGGTGGCGAT GGTCGCCACC AAACAAACGG CCTAGTTCTC

1251   CTACCAACTC TTTTTCCGAA GGTAACTGGC TTCAGCAGAG CGCAGATACC
       GATGGTTGAG AAAAAGGCTT CCATTGACCG AAGTCGTCTC GCGTCTATGG
                                        Eco57I
                                        ~~~~~~~

1301   AAATACTGTC CTTCTAGTGT AGCCGTAGTT AGGCCACCAC TTCAAGAACT
       TTTATGACAG GAAGATCACA TCGGCATCAA TCCGGTGGTG AAGTTCTTGA

1351   CTGTAGCACC GCCTACATAC CTCGCTCTGC TAATCCTGTT ACCAGTGGCT
       GACATCGTGG CGGATGTATG GAGCGAGACG ATTAGGACAA TGGTCACCGA
```

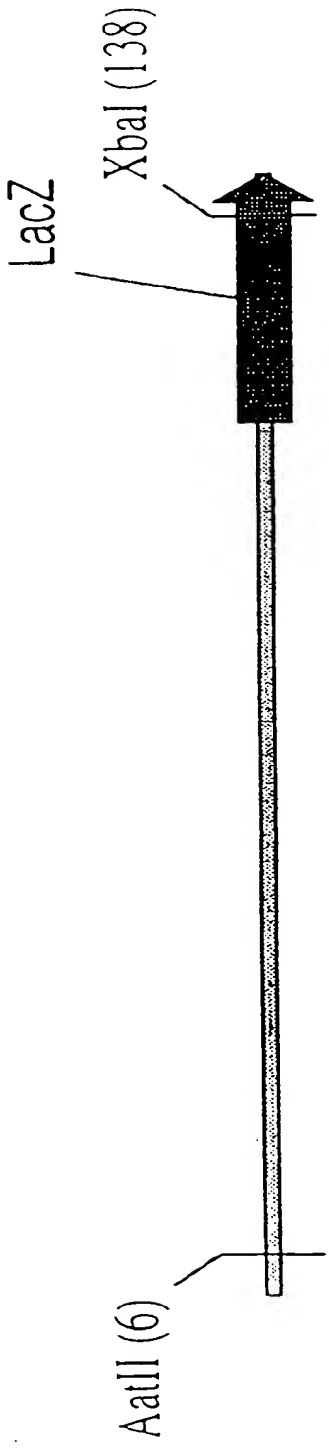
FIG. 28E

```
1401  GCTGCCAGTG GCGATAAGTC GTGTCTTACC GGGTTGGACT CAAGACGATA
      CGACGGTCAC CGCTATTCAG CACAGAATGG CCCAACCTGA GTTCTGCTAT

1451  GTTACCGGAT AAGGCGCAGC GGTCGGGCTG AACGGGGGGT TCGTGCACAC
      CAATGGCCTA TTCCGCGTCG CCAGCCCGAC TTGCCCCCCA AGCACGTGTG

1501  AGCCCAGCTT GGAGCGAACG ACCTACACCG AACTGAGATA CCTACAGCGT
      TCGGGTCGAA CCTCGCTTGC TGGATGTGGC TTGACTCTAT GGATGTCGCA

1551  GAGCTATGAG AAAGCGCCAC GCTTCCCGAA GGGAGAAAGG CGGACAGGTA
      CTCGATACTC TTTCGCGGTG CGAAGGGCTT CCCTCTTTCC GCCTGTCCAT

1601  TCCGGTAAGC GGCAGGGTCG GAACAGGAGA GCGCACGAGG GAGCTTCCAG
      AGGCCATTCG CCGTCCCAGC CTTGTCCTCT CGCGTGCTCC CTCGAAGGTC
                                          BssSI
                                          ~~~~~~

1651  GGGGAAACGC CTGGTATCTT TATAGTCCTG TCGGGTTTCG CCACCTCTGA
      CCCCTTTGCG GACCATAGAA ATATCAGGAC AGCCCAAAGC GGTGGAGACT

1701  CTTGAGCGTC GATTTTTGTG ATGCTCGTCA GGGGGGCGGA GCCTATGGAA
      GAACTCGCAG CTAAAAACAC TACGAGCAGT CCCCCCGCCT CGGATACCTT

1751  AAACGCCAGC AACGCGGCCT TTTTACGGTT CCTGGCCTTT TGCTGGCCTT
```

FIG. 28F

```
        TTTGCGGTCG TTGCGCCGGA AAAATGCCAA GGACCGGAAA ACGACCGGAA

                     HindIII                PacI                BsrGI
                     ~~~~~~                 ~~~~~~~~~           ~~~~
1801    TTGCTCACAT GTAAGCTTCC CCCCCCCCTT AATTAACCCC CCCCCCTGTA
        AACGAGTGTA CATTCGAAGG GGGGGGGGAA TTAATTGGGG GGGGGGACAT

        BsrGI          NheI                BglII                AatII
        ~~             ~~~~~~              ~~~~~~~              ~~~~~~
1851    CACCCCCCCC CCGCTAGCCC CCCCCCCCAG ATCTCCCCCC CCCCGACGTC
        GTGGGGGGGG GGCGATCGGG GGGGGGGGTC TAGAGGGGGG GGGGCTGCAG

              XbaI                   SphI                EcoRI
              ~~~~~~~                ~~~~~~              ~~~~~~~
1901    CCCCCTCTAG ACCCCCCCCC CGCATGCCCC CCCCCCCGAA TTCACGT
        GGGGGAGATC TGGGGGGGGG GCGTACGGGG GGGGGGGCTT AAGTGCA
```

FIG. 28G

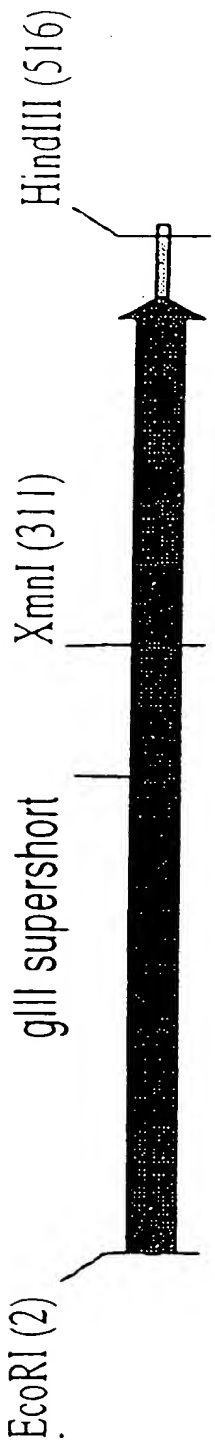


M1
142 bp

FIG. 29A

```
      AatII
      ~~~~~~
  1   GACGTCTTAA TGTGAGTTAG CTCACTCATT AGGCACCCCA GGCTTTACAC
      CTGCAGAATT ACACTCAATC GAGTGAGTAA TCCGTGGGGT CCGAAATGTG

 51   TTTATGCTTC CGGCTCGTAT GTTGTGTGGA ATTGTGAGCG GATAACAATT
      AAATACGAAG GCCGAGCATA CAACACACCT TAACACTCGC CTATTGTTAA

                                                 XbaI
                                                 ~~~~~~
101   TCACACAGGA AACAGCTATG ACCATGATTA CGAATTTCTA GA
      AGTGTGTCCT TTGTCGATAC TGGTACTAAT GCTTAAAGAT CT
```

FIG. 29B



M7-III (ss/myc/TAG)
520 bp

FIG. 30A

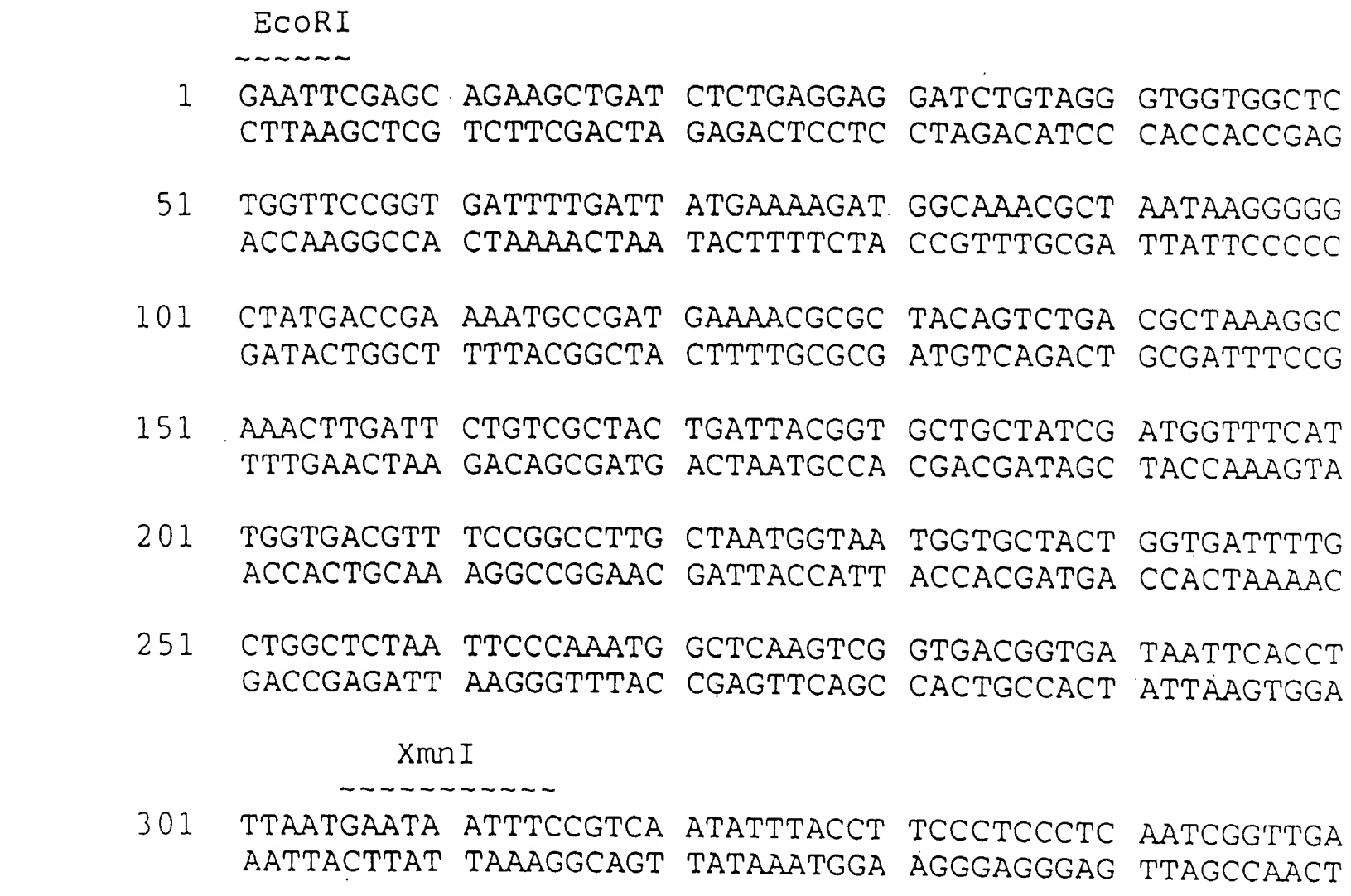
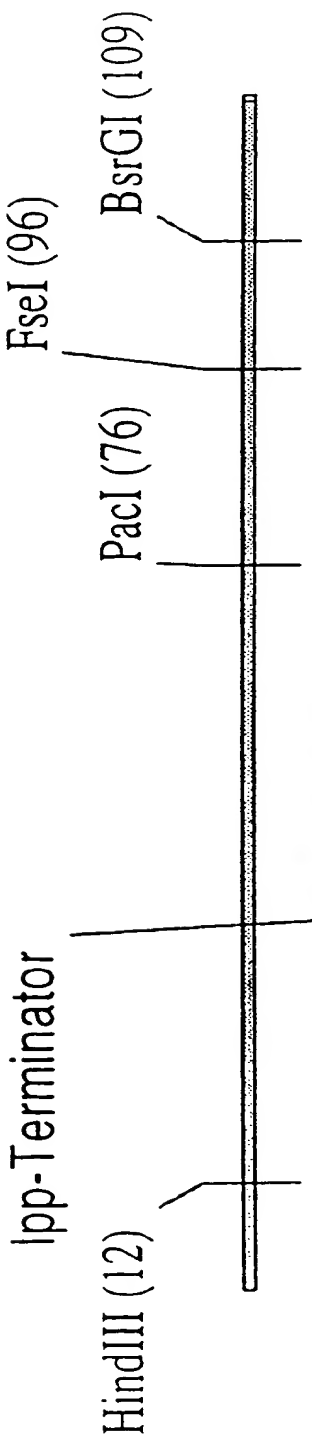

EcoRI
1 GAATTCGAGC AGAAGCTGAT CTCTGAGGAG GATCTGTAGG GTGGTGGCTC
CTTAAGCTCG TCTTCGACTA GAGACTCCTC CTAGACATCC CACCACCGAG
51 TGGTTCCGGT GATTTTGATT ATGAAAAGAT GGCAAACGCT AATAAGGGGG
ACCAAGGCCA CTAAAACTAA TACTTTTCTA CCGTTTGCGA TTATTCCCCC
101 CTATGACCGA AAATGCCGAT GAAAACGCGC TACAGTCTGA CGCTAAAGGC
GATACTGGCT TTTACGGCTA CTTTTGCGCG ATGTCAGACT GCGATTTCCG
151 AAACTTGATT CTGTCGCTAC TGATTACGGT GCTGCTATCG ATGGTTTCAT
TTTGAACTAA GACAGCGATG ACTAATGCCA CGACGATAGC TACCAAAGTA
201 TGGTGACGTT TCCGGCCTTG CTAATGGTAA TGGTGCTACT GGTGATTTTG
ACCACTGCAA AGGCCGGAAC GATTACCATT ACCACGATGA CCACTAAAAC
251 CTGGCTCTAA TTCCCAAATG GCTCAAGTCG GTGACGGTGA TAATTCACCT
GACCGAGATT AAGGGTTTAC CGAGTTCAGC CACTGCCACT ATTAAGTGGA
XmnI
301 TTAATGAATA ATTTCCGTCA ATATTTACCT TCCCTCCCTC AATCGGTTGA
AATTACTTAT TAAAGGCAGT TATAAATGGA AGGGAGGGAG TTAGCCAACT

FIG. 30B

```
351   ATGTCGCCCT TTTGTCTTTG GCGCTGGTAA ACCATATGAA TTTTCTATTG
      TACAGCGGGA AAACAGAAAC CGCGACCATT TGGTATACTT AAAAGATAAC

401   ATTGTGACAA AATAAACTTA TTCCGTGGTG TCTTTGCGTT TCTTTTATAT
      TAACACTGTT TTATTTGAAT AAGGCACCAC AGAAACGCAA AGAAAATATA

451   GTTGCCACCT TTATGTATGT ATTTTCTACG TTTGCTAACA TACTGCGTAA
      CAACGGTGGA AATACATACA TAAAAGATGC AAACGATTGT ATGACGCATT

                      HindIII
                      ~~~~~~
501   TAAGGAGTCT TGATAAGCTT
      ATTCCTCAGA ACTATTCGAA
```

FIG. 30C



M9-II
123 bp

FIG. 31A

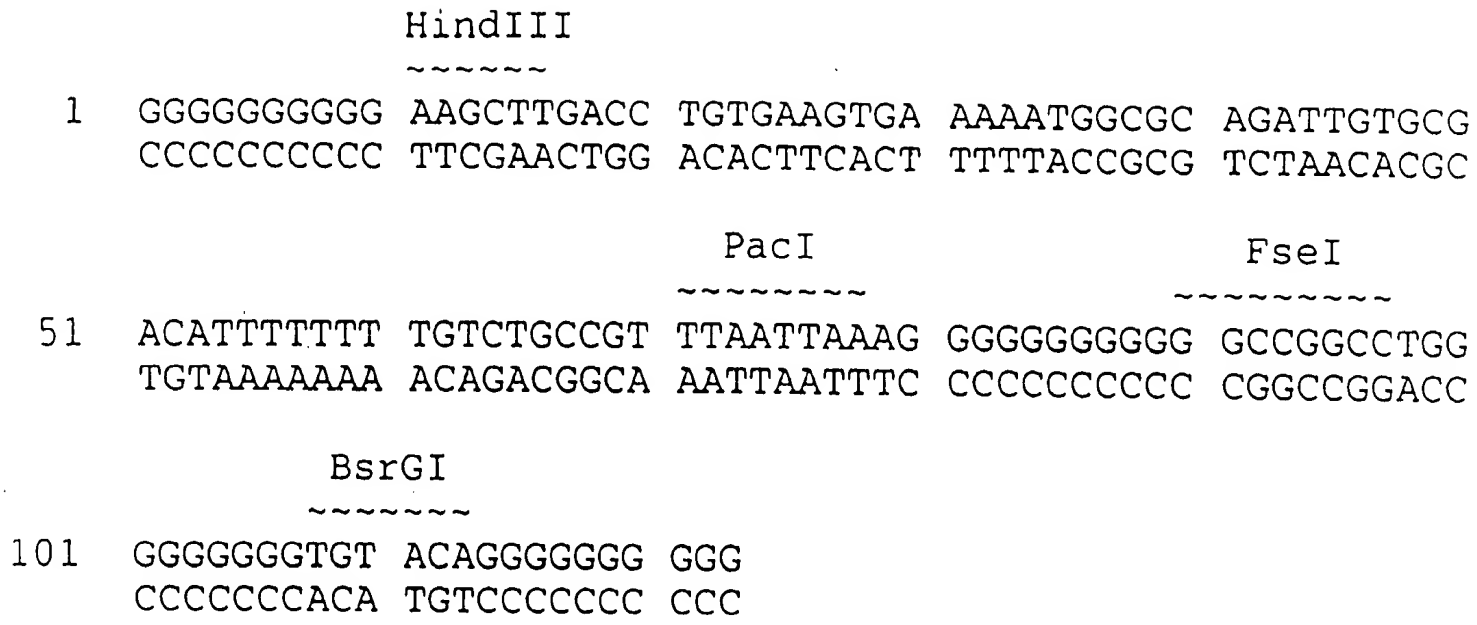
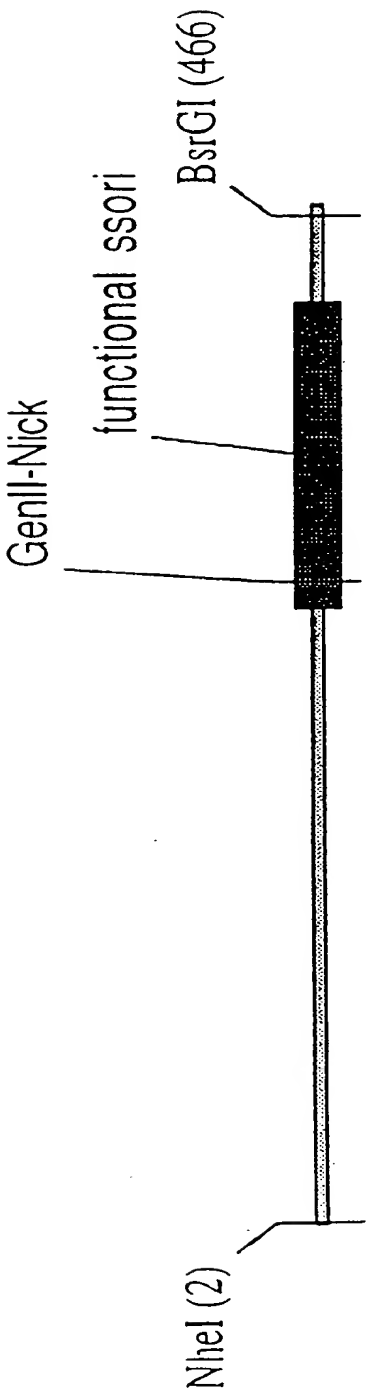

HindIII
1 GGGGGGGGGG AAGCTTGACC TGTGAAGTGA AAAATGGCGC AGATTGTGCG
CCCCCCCCCC TTCGAACTGG ACACTTCACT TTTTACCGCG TCTAACACGC
PacI
FseI
51 ACATTTTTTT TGTCTGCCGT TTAATTAAAG GGGGGGGGGG GCCGGCCTGG
TGTAAAAAAA ACAGACGGCA AATTAATTTC CCCCCCCCCC CGGCCGGACC
BsrGI
101 GGGGGGGTGT ACAGGGGGGG GGG
CCCCCCCACA TGTCCCCCCC CCC

FIG. 31B



M11-III
470 bp

FIG. 32A

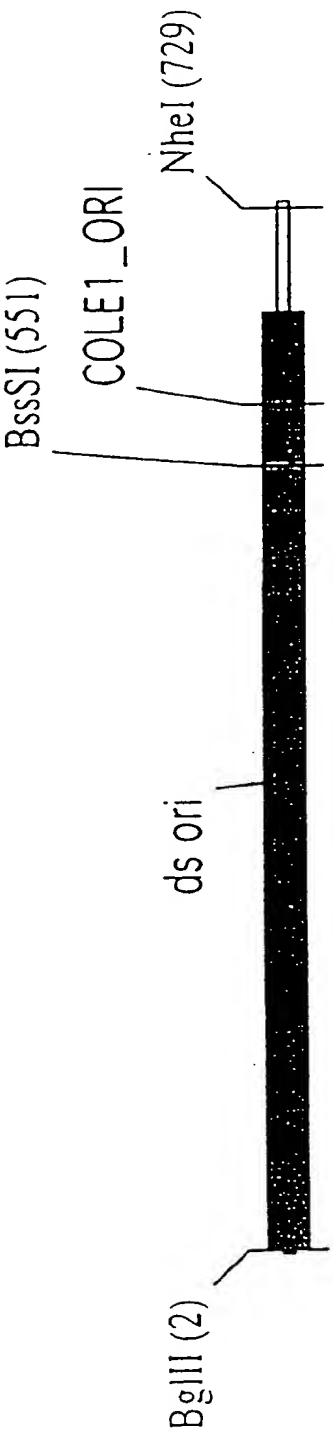
NheI
~~~~~~

```
  1  GCTAGCACGC GCCCTGTAGC GGCGCATTAA GCGCGGCGGG TGTGGTGGTT
     CGATCGTGCG CGGGACATCG CCGCGTAATT CGCGCCGCCC ACACCACCAA

 51  ACGCGCAGCG TGACCGCTAC ACTTGCCAGC GCCCTAGCGC CCGCTCCTTT
     TGCGCGTCGC ACTGGCGATG TGAACGGTCG CGGGATCGCG GGCGAGGAAA

101  CGCTTTCTTC CCTTCCTTTC TCGCCACGTT CGCCGGCTTT CCCCGTCAAG
     GCGAAAGAAG GGAAGGAAAG AGCGGTGCAA GCGGCCGAAA GGGGCAGTTC

151  CTCTAAATCG GGGCATCCCT TTAGGGTTCC GATTTAGTGC TTTACGGCAC
     GAGATTTAGC CCCGTAGGGA AATCCCAAGG CTAAATCACG AAATGCCGTG

201  CTCGACCCCA AAAAACTTGA TTAGGGTGAT GGTTCTCGTA GTGGGCCATC
     GAGCTGGGGT TTTTTGAACT AATCCCACTA CCAAGAGCAT CACCCGGTAG

251  GCCCTGATAG ACGGTTTTTC GCCCTTTGAC GTTGGAGTCC ACGTTCTTTA
     CGGGACTATC TGCCAAAAAG CGGGAAACTG CAACCTCAGG TGCAAGAAAT

301  ATAGTGGACT CTTGTTCCAA ACTGGAACAA CACTCAACCC TATCTCGGTC
     TATCACCTGA GAACAAGGTT TGACCTTGTT GTGAGTTGGG ATAGAGCCAG

351  TATTCTTTTG ATTTATAAGG GATTTTGCCG ATTTCGGCCT ATTGGTTAAA
```

FIG. 32B
~~~~~~

```
      ATAAGAAAAC TAAATATTCC CTAAAACGGC TAAAGCCGGA TAACCAATTT

401   AAATGAGCTG ATTTAACAAA AATTTAACGC GAATTTTAAC AAAATATTAA
      TTTACTCGAC TAAATTGTTT TTAAATTGCG CTTAAAATTG TTTTATAATT

                          BsrGI
                         ~~~~~~~
451   CGTTTACAAT TTCATGTACA
      GCAAATGTTA AAGTACATGT
```

FIG. 32C



M14-EXT2
733 bp

FIG. 33A

BglII
~~~~~~

```
  1  AGATCTGACC AAAATCCCTT AACGTGAGTT TTCGTTCCAC TGAGCGTCAG
     TCTAGACTGG TTTTAGGGAA TTGCACTCAA AAGCAAGGTG ACTCGCAGTC

 51  ACCCCGTAGA AAAGATCAAA GGATCTTCTT GAGATCCTTT TTTTCTGCGC
     TGGGGCATCT TTTCTAGTTT CCTAGAAGAA CTCTAGGAAA AAAAGACGCG

101  GTAATCTGCT GCTTGCAAAC AAAAAAACCA CCGCTACCAG CGGTGGTTTG
     CATTAGACGA CGAACGTTTG TTTTTTTGGT GGCGATGGTC GCCACCAAAC

151  TTTGCCGGAT CAAGAGCTAC CAACTCTTTT TCCGAAGGTA ACTGGCTACA
     AAACGGCCTA GTTCTCGATG GTTGAGAAAA AGGCTTCCAT TGACCGATGT

201  GCAGAGCGCA GATACCAAAT ACTGTTCTTC TAGTGTAGCC GTAGTTAGGC
     CGTCTCGCGT CTATGGTTTA TGACAAGAAG ATCACATCGG CATCAATCCG

251  CACCACTTCA AGAACTCTGT AGCACCGCCT ACATACCTCG CTCTGCTAAT
     GTGGTGAAGT TCTTGAGACA TCGTGGCGGA TGTATGGAGC GAGACGATTA

301  CCTGTTACCA GTGGCTGCTG CCAGTGGCGA TAAGTCGTGT CTTACCGGGT
     GGACAATGGT CACCGACGAC GGTCACCGCT ATTCAGCACA GAATGGCCCA

351  TGGACTCAAG ACGATAGTTA CCGGATAAGG CGCAGCGGTC GGGCTGAACG
```

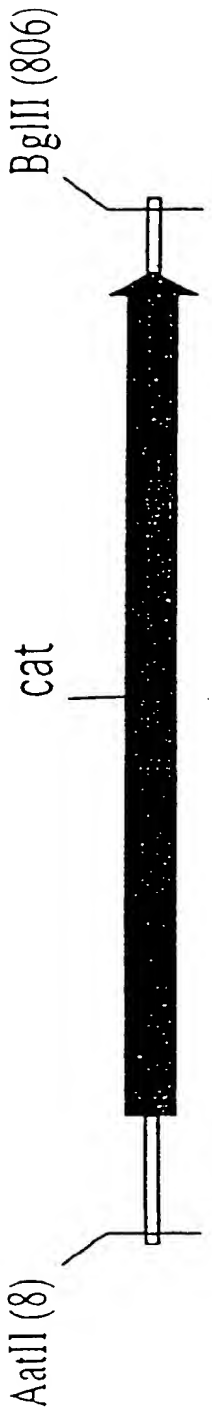
FIG. 33B
~~~~~~

```
      ACCTGAGTTC TGCTATCAAT GGCCTATTCC GCGTCGCCAG CCCGACTTGC

401   GGGGGTTCGT GCACACAGCC CAGCTTGGAG CGAACGACCT ACACCGAACT
      CCCCCAAGCA CGTGTGTCGG GTCGAACCTC GCTTGCTGGA TGTGGCTTGA

451   GAGATACCTA CAGCGTGAGC TATGAGAAAG CGCCACGCTT CCCGAAGGGA
      CTCTATGGAT GTCGCACTCG ATACTCTTTC GCGGTGCGAA GGGCTTCCCT

501   GAAAGGCGGA CAGGTATCCG GTAAGCGGCA GGGTCGGAAC AGGAGAGCGC
      CTTTCCGCCT GTCCATAGGC CATTCGCCGT CCCAGCCTTG TCCTCTCGCG
                                                    BssSI
                                                      ~

551   ACGAGGGAGC TTCCAGGGGG AAACGCCTGG TATCTTTATA GTCCTGTCGG
      TGCTCCCTCG AAGGTCCCCC TTTGCGGACC ATAGAAATAT CAGGACAGCC
      BssSI
      ~~~~~

601   GTTTCGCCAC CTCTGACTTG AGCGTCGATT TTTGTGATGC TCGTCAGGGG
      CAAAGCGGTG GAGACTGAAC TCGCAGCTAA AAACACTACG AGCAGTCCCC

651   GGCGGAGCCT ATGGAAAAAC GCCAGCAACG CGGCCTTTTT ACGGTTCCTG
      CCGCCTCGGA TACCTTTTTG CGGTCGTTGC GCCGGAAAAA TGCCAAGGAC
```

FIG. 33C

```
                                                    NheI
                                                    ~~~~~~
701   GCCTTTTGCT GGCCTTT GC TCACATGGCT AGC
      CGGAAAACGA CCGGAAAACG AGTGTACCGA TCG
```

FIG. 33D



M17
813 bp

FIG. 34A

AatII
~~~~~~

```
  1  GGGACGTCGG GTGAGGTTCC AACTTTCACC ATAATGAAAT AAGATCACTA
     CCCTGCAGCC CACTCCAAGG TTGAAAGTGG TATTACTTTA TTCTAGTGAT

 51  CCGGGCGTAT TTTTTGAGTT ATCGAGATTT TCAGGAGCTA AGGAAGCTAA
     GGCCCGCATA AAAAACTCAA TAGCTCTAAA AGTCCTCGAT TCCTTCGATT

101  AATGGAGAAA AAAATCACTG GATATACCAC CGTTGATATA TCCCAATGGC
     TTACCTCTTT TTTTAGTGAC CTATATGGTG GCAACTATAT AGGGTTACCG

151  ATCGTAAAGA ACATTTTGAG GCATTTCAGT CAGTTGCTCA ATGTACCTAT
     TAGCATTTCT TGTAAAACTC CGTAAAGTCA GTCAACGAGT TACATGGATA

201  AACCAGACCG TTCAGCTGGA TATTACGGCC TTTTTAAAGA CCGTAAAGAA
     TTGGTCTGGC AAGTCGACCT ATAATGCCGG AAAAATTTCT GGCATTTCTT

251  AAATAAGCAC AAGTTTTATC CGGCCTTTAT TCACATTCTT GCCCGCCTGA
     TTTATTCGTG TTCAAAATAG GCCGGAAATA AGTGTAAGAA CGGGCGGACT

301  TGAATGCTCA CCCGGAGTTC CGTATGGCAA TGAAAGACGG TGAGCTGGTG
     ACTTACGAGT GGGCCTCAAG GCATACCGTT ACTTTCTGCC ACTCGACCAC

351  ATATGGGATA GTGTTCACCC TTGTTACACC GTTTTCCATG AGCAAACTGA
```

FIG. 34B
~~~~~~

```
     TATACCCTAT CACAAGTGGG AACAATGTGG CAAAAGGTAC TCGTTTGACT

401  AACGTTTTCA TCGCTCTGGA GTGAATACCA CGACGATTTC CGGCAGTTTC
     TTGCAAAAGT AGCGAGACCT CACTTATGGT GCTGCTAAAG GCCGTCAAAG

451  TACACATATA TTCGCAAGAT GTGGCGTGTT ACGGTGAAAA CCTGGCCTAT
     ATGTGTATAT AAGCGTTCTA CACCGCACAA TGCCACTTTT GGACCGGATA

501  TTCCCTAAAG GGTTTATTGA GAATATGTTT TTCGTCTCAG CCAATCCCTG
     AAGGGATTTC CCAAATAACT CTTATACAAA AAGCAGAGTC GGTTAGGGAC

551  GGTGAGTTTC ACCAGTTTTG ATTTAAACGT AGCCAATATG GACAACTTCT
     CCACTCAAAG TGGTCAAAAC TAAATTTGCA TCGGTTATAC CTGTTGAAGA

601  TCGCCCCCGT TTTCACTATG GGCAAATATT ATACGCAAGG CGACAAGGTG
     AGCGGGGGCA AAAGTGATAC CCGTTTATAA TATGCGTTCC GCTGTTCCAC

651  CTGATGCCGC TGGCGATTCA GGTTCATCAT GCCGTTTGTG ATGGCTTCCA
     GACTACGGCG ACCGCTAAGT CCAAGTAGTA CGGCAAACAC TACCGAAGGT

701  TGTCGGCAGA ATGCTTAATG AATTACAACA GTACTGCGAT GAGTGGCAGG
     ACAGCCGTCT TACGAATTAC TTAATGTTGT CATGACGCTA CTCACCGTCC

751  GCGGGGCGTA ATTTTTTTAA GGCAGTTATT GGGTGCCCTT AAACGCCTGG
```

FIG. 34C

```
                CGCCCCGCAT TAAAAAAATT CCGTCAATAA CCCACGGGAA TTTGCGGACC

                     BglII
                     ~~~~~~
801             TGCTAGATCT TCC
                ACGATCTAGA AGG
```

FIG. 34D

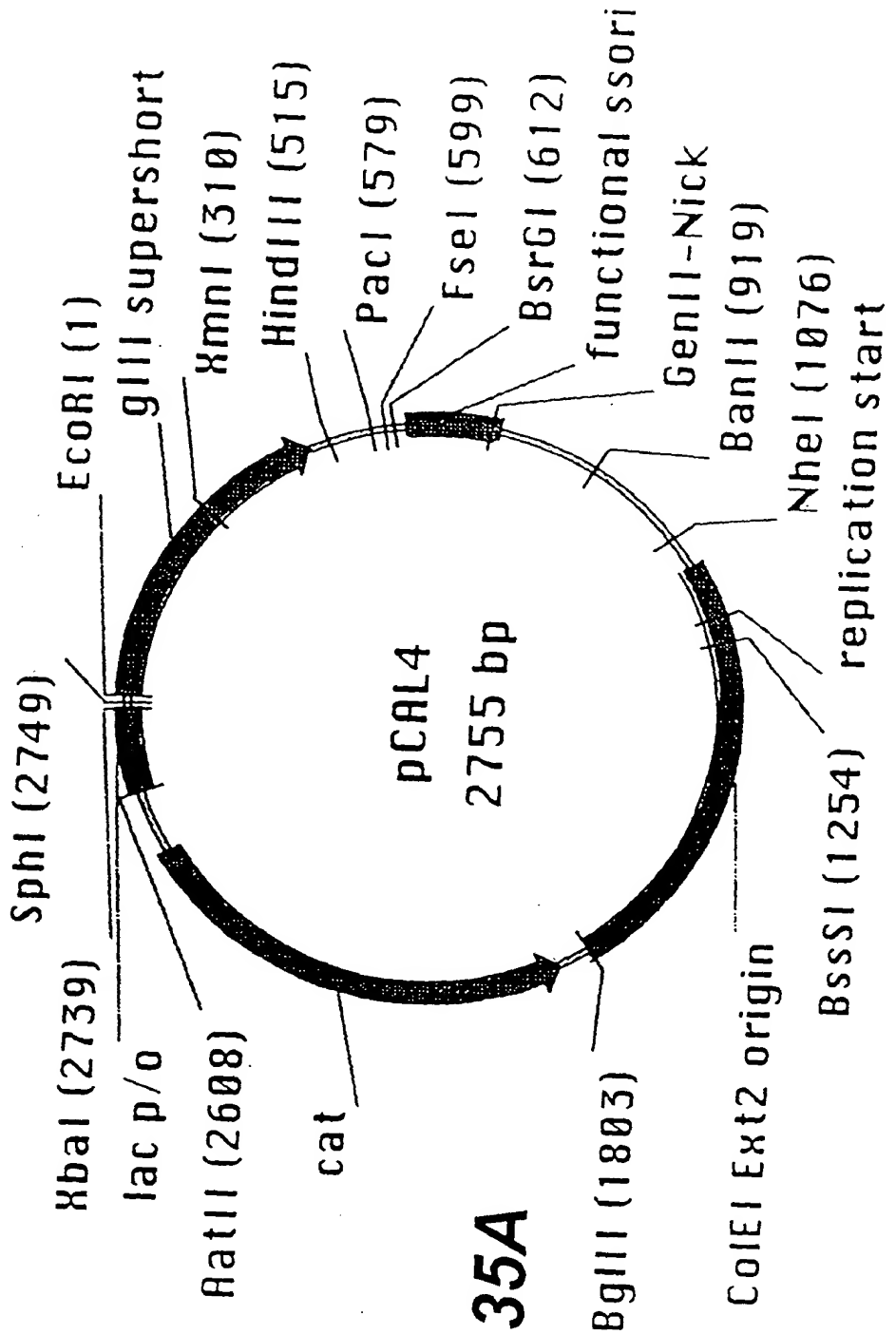

pCAL4
2755 bp
EcoRI (1)
gIII supershort
XmnI (310)
HindIII (515)
PacI (579)
FseI (599)
BsrGI (612)
functional ssori
GenII-Nick
BanII (919)
NheI (1076)
replication start
BssSI (1254)
ColE1 Ext2 origin
BglII (1803)
cat
AatII (2608)
lac p/o
XbaI (2739)
SphI (2749)

FIG. 35A

```
      EcoRI
      ~~~~~
  1   AATTCGAGCA GAAGCTGATC TCTGAGGAGG ATCTGTAGGG TGGTGGCTCT
      TTAAGCTCGT CTTCGACTAG AGACTCCTCC TAGACATCCC ACCACCGAGA

 51   GGTTCCGGTG ATTTTGATTA TGAAAAGATG GCAAACGCTA ATAAGGGGGC
      CCAAGGCCAC TAAAACTAAT ACTTTTCTAC CGTTTGCGAT TATTCCCCCG

101   TATGACCGAA AATGCCGATG AAAACGCGCT ACAGTCTGAC GCTAAAGGCA
      ATACTGGCTT TTACGGCTAC TTTTGCGCGA TGTCAGACTG CGATTTCCGT

151   AACTTGATTC TGTCGCTACT GATTACGGTG CTGCTATCGA TGGTTTCATT
      TTGAACTAAG ACAGCGATGA CTAATGCCAC GACGATAGCT ACCAAAGTAA

201   GGTGACGTTT CCGGCCTTGC TAATGGTAAT GGTGCTACTG GTGATTTTGC
      CCACTGCAAA GGCCGGAACG ATTACCATTA CCACGATGAC CACTAAAACG

251   TGGCTCTAAT TCCCAAATGG CTCAAGTCGG TGACGGTGAT AATTCACCTT
      ACCGAGATTA AGGGTTTACC GAGTTCAGCC ACTGCCACTA TTAAGTGGAA

            XmnI
          ~~~~~~~~~~~
301   TAATGAATAA TTTCCGTCAA TATTTACCTT CCCTCCCTCA ATCGGTTGAA
      ATTACTTATT AAAGGCAGTT ATAAATGGAA GGGAGGGAGT TAGCCAACTT
```

FIG. 35B

```
351  TGTCGCCCTT TTGTCTTTGG CGCTGGTAAA CCATATGAAT TTTCTATTGA
     ACAGCGGGAA AACAGAAACC GCGACCATTT GGTATACTTA AAAGATAACT

401  TTGTGACAAA ATAAACTTAT TCCGTGGTGT CTTTGCGTTT CTTTTATATG
     AACACTGTTT TATTTGAATA AGGCACCACA GAAACGCAAA GAAAATATAC

451  TTGCCACCTT TATGTATGTA TTTTCTACGT TTGCTAACAT ACTGCGTAAT
     AACGGTGGAA ATACATACAT AAAAGATGCA AACGATTGTA TGACGCATTA

                HindIII
                ~~~~~~
501  AAGGAGTCTT GATAAGCTTG ACCTGTGAAG TGAAAAATGG CGCAGATTGT
     TTCCTCAGAA CTATTCGAAC TGGACACTTC ACTTTTTACC GCGTCTAACA

                                  PacI                 FseI
                                  ~~~~~~~~~~           ~~~~~~~~
551  GCGACATTTT TTTTGTCTGC CGTTTAATTA AAGGGGGGGG GGGGCCGGCC
     CGCTGTAAAA AAAACAGACG GCAAATTAAT TTCCCCCCCC CCCCGGCCGG

               BsrGI
               ~~~~~~
601  TGGGGGGGGG TGTACATGAA ATTGTAAACG TTAATATTTT GTTAAAATTC
     ACCCCCCCCC ACATGTACTT TAACATTTGC AATTATAAAA CAATTTTAAG
```

FIG. 35C

```
651   GCGTTAAATT TTTGTTAAAT CAGCTCATTT TTTAACCAAT AGGCCGAAAT
      CGCAATTTAA AAACAATTTA GTCGAGTAAA AAATTGGTTA TCCGGCTTTA

701   CGGCAAAATC CCTTATAAAT CAAAAGAATA GACCGAGATA GGGTTGAGTG
      GCCGTTTTAG GGAATATTTA GTTTTCTTAT CTGGCTCTAT CCCAACTCAC

751   TTGTTCCAGT TTGGAACAAG AGTCCACTAT TAAAGAACGT GGACTCCAAC
      AACAAGGTCA AACCTTGTTC TCAGGTGATA ATTTCTTGCA CCTGAGGTTG

801   GTCAAAGGGC GAAAAACCGT CTATCAGGGC GATGGCCCAC TACGAGAACC
      CAGTTTCCCG CTTTTTGGCA GATAGTCCCG CTACCGGGTG ATGCTCTTGG

851   ATCACCCTAA TCAAGTTTTT TGGGGTCGAG GTGCCGTAAA GCACTAAATC
      TAGTGGGATT AGTTCAAAAA ACCCCAGCTC CACGGCATTT CGTGATTTAG

                        BanII
                        ~~~~~~
901   GGAACCCTAA AGGGAGCCCC CGATTTAGAG CTTGACGGGG AAAGCCGGCG
      CCTTGGGATT TCCCTCGGGG GCTAAATCTC GAACTGCCCC TTTCGGCCGC

951   AACGTGGCGA GAAAGGAAGG GAAGAAAGCG AAAGGAGCGG GCGCTAGGGC
      TTGCACCGCT CTTTCCTTCC CTTCTTTCGC TTTCCTCGCC CGCGATCCCG
```

FIG. 35D

```
1001  GCTGGCAAGT GTAGCGGTCA CGCTGCGCGT AACCACCACA CCCGCCGCGC
      CGACCGTTCA CATCGCCAGT GCGACGCGCA TTGGTGGTGT GGGCGGCGCG

                                    NheI
                                    ~~~~~~
1051  TTAATGCGCC GCTACAGGGC GCGTGCTAGC CATGTGAGCA AAAGGCCAGC
      AATTACGCGG CGATGTCCCG CGCACGATCG GTACACTCGT TTTCCGGTCG

1101  AAAAGGCCAG GAACCGTAAA AAGGCCGCGT TGCTGGCGTT TTTCCATAGG
      TTTTCCGGTC CTTGGCATTT TTCCGGCGCA ACGACCGCAA AAAGGTATCC

1151  CTCCGCCCCC CTGACGAGCA TCACAAAAAT CGACGCTCAA GTCAGAGGTG
      GAGGCGGGGG GACTGCTCGT AGTGTTTTTA GCTGCGAGTT CAGTCTCCAC

1201  GCGAAACCCG ACAGGACTAT AAAGATACCA GGCGTTTCCC CCTGGAAGCT
      CGCTTTGGGC TGTCCTGATA TTTCTATGGT CCGCAAAGGG GGACCTTCGA

        BssSI
        ~~~~~~
1251  CCCTCGTGCG CTCTCCTGTT CCGACCCTGC CGCTTACCGG ATACCTGTCC
      GGGAGCACGC GAGAGGACAA GGCTGGGACG GCGAATGGCC TATGGACAGG

1301  GCCTTTCTCC CTTCGGGAAG CGTGGCGCTT TCTCATAGCT CACGCTGTAG
      CGGAAAGAGG GAAGCCCTTC GCACCGCGAA AGAGTATCGA GTGCGACATC
```

FIG. 35E

```
1351  GTATCTCAGT TCGGTGTAGG TCGTTCGCTC CAAGCTGGGC TGTGTGCACG
      CATAGAGTCA AGCCACATCC AGCAAGCGAG GTTCGACCCG ACACACGTGC

1401  AACCCCCCGT TCAGCCCGAC CGCTGCGCCT TATCCGGTAA CTATCGTCTT
      TTGGGGGGCA AGTCGGGCTG GCGACGCGGA ATAGGCCATT GATAGCAGAA

1451  GAGTCCAACC CGGTAAGACA CGACTTATCG CCACTGGCAG CAGCCACTGG
      CTCAGGTTGG GCCATTCTGT GCTGAATAGC GGTGACCGTC GTCGGTGACC

1501  TAACAGGATT AGCAGAGCGA GGTATGTAGG CGGTGCTACA GAGTTCTTGA
      ATTGTCCTAA TCGTCTCGCT CCATACATCC GCCACGATGT CTCAAGAACT

1551  AGTGGTGGCC TAACTACGGC TACACTAGAA GAACAGTATT TGGTATCTGC
      TCACCACCGG ATTGATGCCG ATGTGATCTT CTTGTCATAA ACCATAGACG

1601  GCTCTGCTGT AGCCAGTTAC CTTCGGAAAA AGAGTTGGTA GCTCTTGATC
      CGAGACGACA TCGGTCAATG GAAGCCTTTT TCTCAACCAT CGAGAACTAG

1651  CGGCAAACAA ACCACCGCTG GTAGCGGTGG TTTTTTTGTT TGCAAGCAGC
      GCCGTTTGTT TGGTGGCGAC CATCGCCACC AAAAAAACAA ACGTTCGTCG

1701  AGATTACGCG CAGAAAAAAA GGATCTCAAG AAGATCCTTT GATCTTTTCT
      TCTAATGCGC GTCTTTTTTT CCTAGAGTTC TTCTAGGAAA CTAGAAAAGA
```

FIG. 35F

```
1751  ACGGGGTCTG ACGCTCAGTG GAACGAAAAC TCACGTTAAG GGATTTTGGT
      TGCCCCAGAC TGCGAGTCAC CTTGCTTTTG AGTGCAATTC CCTAAAACCA

        BglII
       ~~~~~~
1801  CAGATCTAGC ACCAGGCGTT TAAGGGCACC AATAACTGCC TTAAAAAAAT
      GTCTAGATCG TGGTCCGCAA ATTCCCGTGG TTATTGACGG AATTTTTTTA

1851  TACGCCCCGC CCTGCCACTC ATCGCAGTAC TGTTGTAATT CATTAAGCAT
      ATGCGGGGCG GGACGGTGAG TAGCGTCATG ACAACATTAA GTAATTCGTA

1901  TCTGCCGACA TGGAAGCCAT CACAAACGGC ATGATGAACC TGAATCGCCA
      AGACGGCTGT ACCTTCGGTA GTGTTTGCCG TACTACTTGG ACTTAGCGGT

1951  GCGGCATCAG CACCTTGTCG CCTTGCGTAT AATATTTGCC CATAGTGAAA
      CGCCGTAGTC GTGGAACAGC GGAACGCATA TTATAAACGG GTATCACTTT

2001  ACGGGGGCGA AGAAGTTGTC CATATTGGCT ACGTTTAAAT CAAAACTGGT
      TGCCCCCGCT TCTTCAACAG GTATAACCGA TGCAAATTTA GTTTTGACCA

2051  GAAACTCACC CAGGGATTGG CTGAGACGAA AAACATATTC TCAATAAACC
      CTTTGAGTGG GTCCCTAACC GACTCTGCTT TTTGTATAAG AGTTATTTGG
```

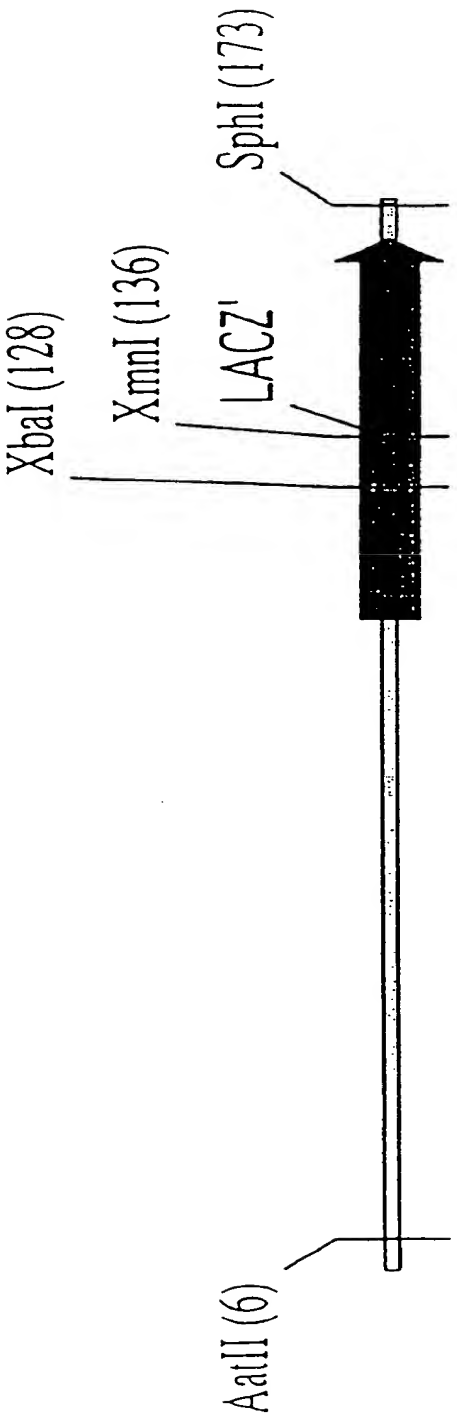
FIG. 35G

```
2101  CTTTAGGGAA ATAGGCCAGG TTTTCACCGT AACACGCCAC ATCTTGCGAA
      GAAATCCCTT TATCCGGTCC AAAAGTGGCA TTGTGCGGTG TAGAACGCTT

2151  TATATGTGTA GAAACTGCCG GAAATCGTCG TGGTATTCAC TCCAGAGCGA
      ATATACACAT CTTTGACGGC CTTTAGCAGC ACCATAAGTG AGGTCTCGCT

2201  TGAAAACGTT TCAGTTTGCT CATGGAAAAC GGTGTAACAA GGGTGAACAC
      ACTTTTGCAA AGTCAAACGA GTACCTTTTG CCACATTGTT CCCACTTGTG

2251  TATCCCATAT CACCAGCTCA CCGTCTTTCA TTGCCATACG GAACTCCGGG
      ATAGGGTATA GTGGTCGAGT GGCAGAAAGT AACGGTATGC CTTGAGGCCC

2301  TGAGCATTCA TCAGGCGGGC AAGAATGTGA ATAAAGGCCG GATAAAACTT
      ACTCGTAAGT AGTCCGCCCG TTCTTACACT TATTTCCGGC CTATTTTGAA

2351  GTGCTTATTT TTCTTTACGG TCTTTAAAAA GGCCGTAATA TCCAGCTGAA
      CACGAATAAA AAGAAATGCC AGAAATTTTT CCGGCATTAT AGGTCGACTT

2401  CGGTCTGGTT ATAGGTACAT TGAGCAACTG ACTGAAATGC CTCAAAATGT
      GCCAGACCAA TATCCATGTA ACTCGTTGAC TGACTTTACG GAGTTTTACA

2451  TCTTTACGAT GCCATTGGGA TATATCAACG GTGGTATATC CAGTGATTTT
      AGAAATGCTA CGGTAACCCT ATATAGTTGC CACCATATAG GTCACTAAAA
```

FIG. 35H

```
2501  TTTCTCCATT TTAGCTTCCT TAGCTCCTGA AAATCTCGAT AACTCAAAAA
      AAAGAGGTAA AATCGAAGGA ATCGAGGACT TTTAGAGCTA TTGAGTTTTT

2551  ATACGCCCGG TAGTGATCTT ATTTCATTAT GGTGAAAGTT GGAACCTCAC
      TATGCGGGCC ATCACTAGAA TAAAGTAATA CCACTTTCAA CCTTGGAGTG

         AatII
        ~~~~~~
2601  CCGACGTCTA ATGTGAGTTA GCTCACTCAT TAGGCACCCC AGGCTTTACA
      GGCTGCAGAT TACACTCAAT CGAGTGAGTA ATCCGTGGGG TCCGAAATGT

2651  CTTTATGCTT CCGGCTCGTA TGTTGTGTGG AATTGTGAGC GGATAACAAT
      GAAATACGAA GGCCGAGCAT ACAACACACC TTAACACTCG CCTATTGTTA

                                                 XbaI    SphI
                                                ~~~~~~~~~~~~~
2701  TTCACACAGG AAACAGCTAT GACCATGATT ACGAATTTCT AGAGCATGCG
      AAGTGTGTCC TTTGTCGATA CTGGTACTAA TGCTTAAAGA TCTCGTACGC

      EcoRI

2751  GGGGG
      CCCCC
```

FIG. 35I



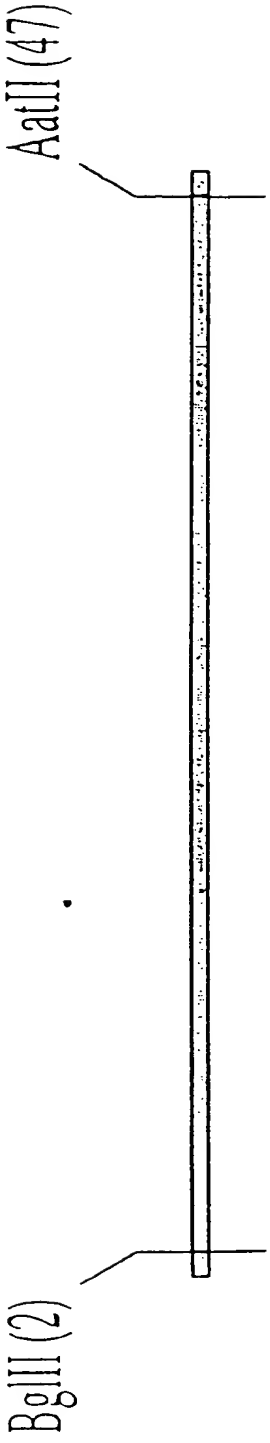
M2
173 bp

FIG. 35J

M 2:

```
          AatII
          ~~~~~~
   1  GACGTCTTAA TGTGAGTTAG CTCACTCATT AGGCACCCCA GGCTTTACAC
      CTGCAGAATT ACACTCAATC GAGTGAGTAA TCCGTGGGGT CCGAAATGTG

  51  TTTATGCTTC CGGCTCGTAT GTTGTGTGGA ATTGTGAGCG GATAACAATT
      AAATACGAAG GCCGAGCATA CAACACACCT TAACACTCGC CTATTGTTAA

                                          XmnI
                                          ~~~~~~~~~~
                                    XbaI
                                    ~~~~~~~
 101  TCACACAGGA AACAGCTATG ACCATGTCTA GAATAACTTC GTATAATGTA
      AGTGTGTCCT TTGTCGATAC TGGTACAGAT CTTATTGAAG CATATTACAT

                          SphI
                          ~~~~~~
 151  CGCTATACGA AGTTATCGCA TGC
      GCGATATGCT TCAATAGCGT ACG
```

FIG. 35K



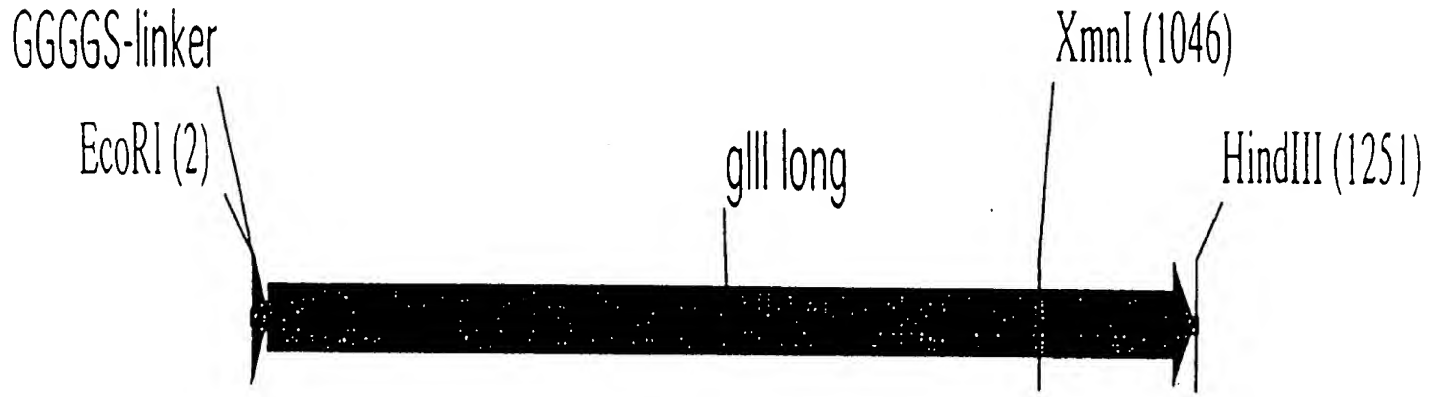
M3
47 bp

FIG. 35L

M 3:

```
    BglII                                                    AatII
    ------                                                   -----
1   AGATCTCATA ACTTCGTATA ATGTATGCTA TACGAAGTTA TGACGTC
    TCTAGAGTAT TGAAGCATAT TACATACGAT ATGCTTCAAT ACTGCAG
```

FIG. 35M



M7-1 (long)

1255 bp

FIG. 35N

M 7-I (long):

```
     EcoRI
     ~~~~~~
  1  GAATTCGGTG GTGGTGGATC TGCGTGCGCT GAAACGGTTG AAAGTTGTTT
     CTTAAGCCAC CACCACCTAG ACGCACGCGA CTTTGCCAAC TTTCAACAAA

 51  AGCAAAATCC CATACAGAAA ATTCATTTAC TAACGTCTGG AAAGACGACA
     TCGTTTTAGG GTATGTCTTT TAAGTAAATG ATTGCAGACC TTTCTGCTGT

101  AAACTTTAGA TCGTTACGCT AACTATGAGG GCTGTCTGTG GAATGCTACA
     TTTGAAATCT AGCAATGCGA TTGATACTCC CGACAGACAC CTTACGATGT

151  GGCGTTGTAG TTTGTACTGG TGACGAAACT CAGTGTTACG GTACATGGGT
     CCGCAACATC AAACATGACC ACTGCTTTGA GTCACAATGC CATGTACCCA

201  TCCTATTGGG CTTGCTATCC CTGAAAATGA GGGTGGTGGC TCTGAGGGTG
     AGGATAACCC GAACGATAGG GACTTTTACT CCCACCACCG AGACTCCCAC

251  GCGGTTCTGA GGGTGGCGGT TCTGAGGGTG GCGGTACTAA ACCTCCTGAG
     CGCCAAGACT CCCACCGCCA AGACTCCCAC CGCCATGATT TGGAGGACTC

301  TACGGTGATA CACCTATTCC GGGCTATACT TATATCAACC CTCTCGACGG
     ATGCCACTAT GTGGATAAGG CCCGATATGA ATATAGTTGG GAGAGCTGCC
```

FIG. 35O

```
351  CACTTATCCG CCTGGTACTG AGCAAAACCC CGCTAATCCT AATCCTTCTC
     GTGAATAGGC GGACCATGAC TCGTTTTGGG GCGATTAGGA TTAGGAAGAG

401  TTGAGGAGTC TCAGCCTCTT AATACTTTCA TGTTTCAGAA TAATAGGTTC
     AACTCCTCAG AGTCGGAGAA TTATGAAAGT ACAAAGTCTT ATTATCCAAG

451  CGAAATAGGC AGGGGGCATT AACTGTTTAT ACGGGCACTG TTACTCAAGG
     GCTTTATCCG TCCCCCGTAA TTGACAAATA TGCCCGTGAC AATGAGTTCC

501  CACTGACCCC GTTAAAACTT ATTACCAGTA CACTCCTGTA TCATCAAAAG
     GTGACTGGGG CAATTTTGAA TAATGGTCAT GTGAGGACAT AGTAGTTTTC

551  CCATGTATGA CGCTTACTGG AACGGTAAAT TCAGAGACTG CGCTTTCCAT
     GGTACATACT GCGAATGACC TTGCCATTTA AGTCTCTGAC GCGAAAGGTA

601  TCTGGCTTTA ATGAGGATTT ATTTGTTTGT GAATATCAAG GCCAATCGTC
     AGACCGAAAT TACTCCTAAA TAAACAAACA CTTATAGTTC CGGTTAGCAG

651  TGACCTGCCT CAACCTCCTG TCAATGCTGG CGGCGGCTCT GGTGGTGGTT
     ACTGGACGGA GTTGGAGGAC AGTTACGACC GCCGCCGAGA CCACCACCAA

701  CTGGTGGCGG CTCTGAGGGT GGTGGCTCTG AGGGTGGCGG TTCTGAGGGT
     GACCACCGCC GAGACTCCCA CCACCGAGAC TCCCACCGCC AAGACTCCCA
```

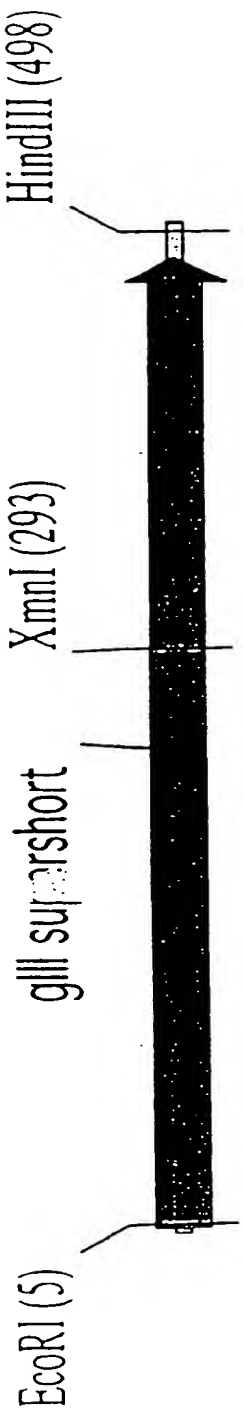
FIG. 35P

```
751  GGCGGCTCTG AGGGAGGCGG TTCCGGTGGT GGCTCTGGTT CCGGTGATTT
     CCGCCGAGAC TCCCTCCGCC AAGGCCACCA CCGAGACCAA GGCCACTAAA

801  TGATTATGAA AAGATGGCAA ACGCTAATAA GGGGGCTATG ACCGAAAATG
     ACTAATACTT TTCTACCGTT TGCGATTATT CCCCCGATAC TGGCTTTTAC

851  CCGATGAAAA CGCGCTACAG TCTGACGCTA AAGGCAAACT TGATTCTGTC
     GGCTACTTTT GCGCGATGTC AGACTGCGAT TTCCGTTTGA ACTAAGACAG

901  GCTACTGATT ACGGTGCTGC TATCGATGGT TTCATTGGTG ACGTTTCCGG
     CGATGACTAA TGCCACGACG ATAGCTACCA AAGTAACCAC TGCAAAGGCC

951  CCTTGCTAAT GGTAATGGTG CTACTGGTGA TTTTGCTGGC TCTAATTCCC
     GGAACGATTA CCATTACCAC GATGACCACT AAAACGACCG AGATTAAGGG

                                                    XmnI
                                                    ~~~~~~~~~~

1001 AAATGGCTCA AGTCGGTGAA GGTGATAATT CACCTTTAAT GAATAATTTC
     TTTACCGAGT TCAGCCACTT CCACTATTAA GTGGAAATTA CTTATTAAAG

1051 CGTCAATATT TACCTTCCAT CCCTCAATCG GTTGAATGTC GCCCTTTTGT
     GCAGTTATAA ATGGAAGGTA GGGAGTTAGC CAACTTACAG CGGGAAAACA
```

FIG. 35Q

```
1101   CTTTGGCGCT GGTAAACCCT ATGAATTTTC TATTGATTGT GACAAAATAA
       GAAACCGCGA CCATTTGGGA TACTTAAAAG ATAACTAACA CTGTTTTATT

1151   ACTTATTCCG TGGTGTCTTT GCGTTTCTTT TATATGTTGC CACCTTTATG
       TGAATAAGGC ACCACAGAAA CGCAAAGAAA ATATACAACG GTGGAAATAC

                                                    HindIII
                                                    ~
1201   TATGTATTTT CTACGTTTGC TAACATACTG CGTAATAAGG AGTCTTGATA
       ATACATAAAA GATGCAAACG ATTGTATGAC GCATTATTCC TCAGAACTAT

       HindI
       ~~~~
1251   AGCTT
       TCGAA
```

FIG. 35R



M7-11 (ss-TAG)
502 bp

FIG. 35S

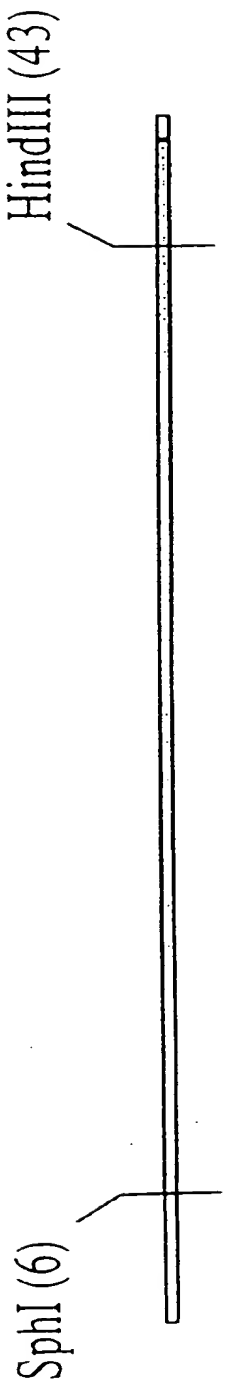
M 7-II (ss-TAG):

```
          EcoRI
          ~~~~~~
   1  CGGGAATTCG GAGGCGGTTC CGGTGGTGGC TCTGGTTCCG GTGATTTTGA
      GCCCTTAAGC CTCCGCCAAG GCCACCACCG AGACCAAGGC CACTAAAACT

  51  TTATGAAAAG ATGGCAAACG CTAATAAGGG GGCTATGACC GAAAATGCCG
      AATACTTTTC TACCGTTTGC GATTATTCCC CCGATACTGG CTTTTACGGC

 101  ATGAAAACGC GCTACAGTCT GACGCTAAAG GCAAACTTGA TTCTGTCGCT
      TACTTTTGCG CGATGTCAGA CTGCGATTTC CGTTTGAACT AAGACAGCGA

 151  ACTGATTACG GTGCTGCTAT CGATGGTTTC ATTGGTGACG TTTCCGGCCT
      TGACTAATGC CACGACGATA GCTACCAAAG TAACCACTGC AAAGGCCGGA

 201  TGCTAATGGT AATGGTGCTA CTGGTGATTT TGCTGGCTCT AATTCCCAAA
      ACGATTACCA TTACCACGAT GACCACTAAA ACGACCGAGA TTAAGGGTTT

                                                    XmnI
                                                    ~~~~~~~~~~~
 251  TGGCTCAAGT CGGTGACGGT GATAATTCAC CTTTAATGAA TAATTTCCGT
      ACCGAGTTCA GCCACTGCCA CTATTAAGTG GAAATTACTT ATTAAAGGCA
```

FIG. 35T

```
301  CAATATTTAC CTTCCCTCCC TCAATCGGTT GAATGTCGCC CTTTTGTCTT
     GTTATAAATG GAAGGGAGGG AGTTAGCCAA CTTACAGCGG GAAAACAGAA

351  TGGCGCTGGT AAACCATATG AATTTTCTAT TGATTGTGAC AAAATAAACT
     ACCGCGACCA TTTGGTATAC TTAAAAGATA ACTAACACTG TTTTATTTGA

401  TATTCCGTGG TGTCTTTGCG TTTCTTTTAT ATGTTGCCAC CTTTATGTAT
     ATAAGGCACC ACAGAAACGC AAAGAAAATA TACAACGGTG GAAATACATA

                                                  HindIII
                                                  ~~~~
451  GTATTTTCTA CGTTTGCTAA CATACTGCGT AATAAGGAGT CTTGATAAGC
     CATAAAAGAT GCAAACGATT GTATGACGCA TTATTCCTCA GAACTATTCG

     Hi
     ~
501  TT
     AA
```

FIG. 35U



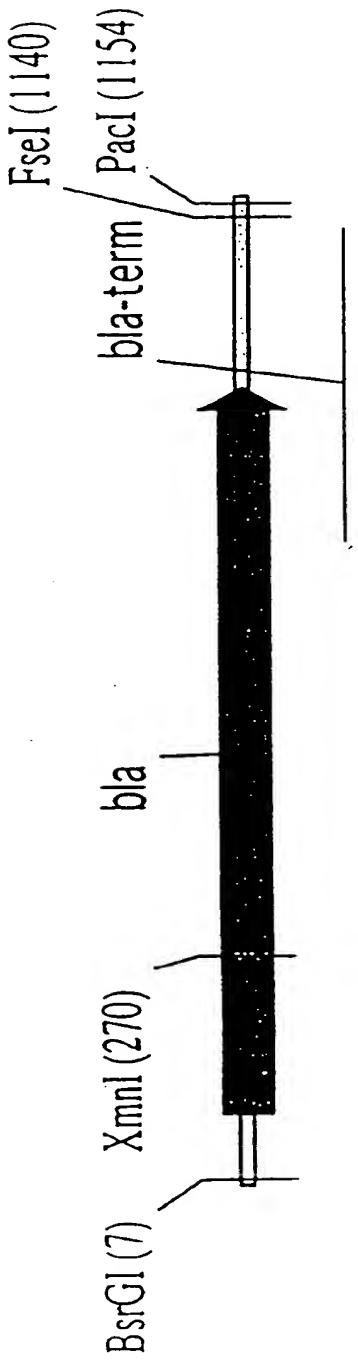
M8
47 bp

FIG. 35V

M 8:

```
    SphI                                                    HindIII
    ~~~~~~                                                   ~~~~~
1   GCATGCCATA ACTTCGTATA ATGTACGCTA TACGAAGTTA TAAGCTT
    CGTACGGTAT TGAAGCATAT TACATGCGAT ATGCTTCAAT ATTCGAA
```

FIG. 35W



M10-11
1163 bp

FIG. 35X

M 10-II:

```
          BsrGI
         ~~~~~~~
   1  GGGGGTGTAC ATTCAAATAT GTATCCGCTC ATGAGACAAT AACCCTGATA
      CCCCCACATG TAAGTTTATA CATAGGCGAG TACTCTGTTA TTGGGACTAT

  51  AATGCTTCAA TAATATTGAA AAAGGAAGAG TATGAGTATT CAACATTTCC
      TTACGAAGTT ATTATAACTT TTTCCTTCTC ATACTCATAA GTTGTAAAGG

 101  GTGTCGCCCT TATTCCCTTT TTTGCGGCAT TTTGCCTTCC TGTTTTTGCT
      CACAGCGGGA ATAAGGGAAA AAACGCCGTA AAACGGAAGG ACAAAAACGA

 151  CACCCAGAAA CGCTGGTGAA AGTAAAAGAT GCTGAGGATC AGTTGGGTGC
      GTGGGTCTTT GCGACCACTT TCATTTTCTA CGACTCCTAG TCAACCCACG

 201  GCGAGTGGGT TACATCGAAC TGGATCTCAA CAGCGGTAAG ATCCTTGAGA
      CGCTCACCCA ATGTAGCTTG ACCTAGAGTT GTCGCCATTC TAGGAACTCT

                        XmnI
                      ~~~~~~~~~~~
 251  GTTTTCGCCC CGAAGAACGT TTTCCAATGA TGAGCACTTT TAAAGTTCTG
      CAAAAGCGGG GCTTCTTGCA AAAGGTTACT ACTCGTGAAA ATTTCAAGAC
```

FIG. 35Y

```
301  CTATGTGGCG CGGTATTATC CCGTATTGAC GCCGGGCAAG AGCAACTCGG
     GATACACCGC GCCATAATAG GGCATAACTG CGGCCCGTTC TCGTTGAGCC

351  TCGCCGCATA CACTATTCTC AGAATGACTT GGTTGAGTAC TCACCAGTCA
     AGCGGCGTAT GTGATAAGAG TCTTACTGAA CCAACTCATG AGTGGTCAGT

401  CAGAAAAGCA TCTTACGGAT GGCATGACAG TAAGAGAATT ATGCAGTGCT
     GTCTTTTCGT AGAATGCCTA CCGTACTGTC ATTCTCTTAA TACGTCACGA

451  GCCATAACCA TGAGTGATAA CACTGCGGCC AACTTACTTC TGACAACGAT
     CGGTATTGGT ACTCACTATT GTGACGCCGG TTGAATGAAG ACTGTTGCTA

501  CGGAGGACCG AAGGAGCTAA CCGCTTTTTT GCACAACATG GGGGATCATG
     GCCTCCTGGC TTCCTCGATT GGCGAAAAAA CGTGTTGTAC CCCCTAGTAC

551  TAACTCGCCT TGATCGTTGG GAACCGGAGC TGAATGAAGC CATACCAAAC
     ATTGAGCGGA ACTAGCAACC CTTGGCCTCG ACTTACTTCG GTATGGTTTG

601  GACGAGCGTG ACACCACGAT GCCTGTAGCA ATGGCAACAA CGTTGCGCAA
     CTGCTCGCAC TGTGGTGCTA CGGACATCGT TACCGTTGTT GCAACGCGTT

651  ACTATTAACT GGCGAACTAC TTACTCTAGC TTCCCGGCAA CAGTTAATAG
     TGATAATTGA CCGCTTGATG AATGAGATCG AAGGGCCGTT GTCAATTATC
```

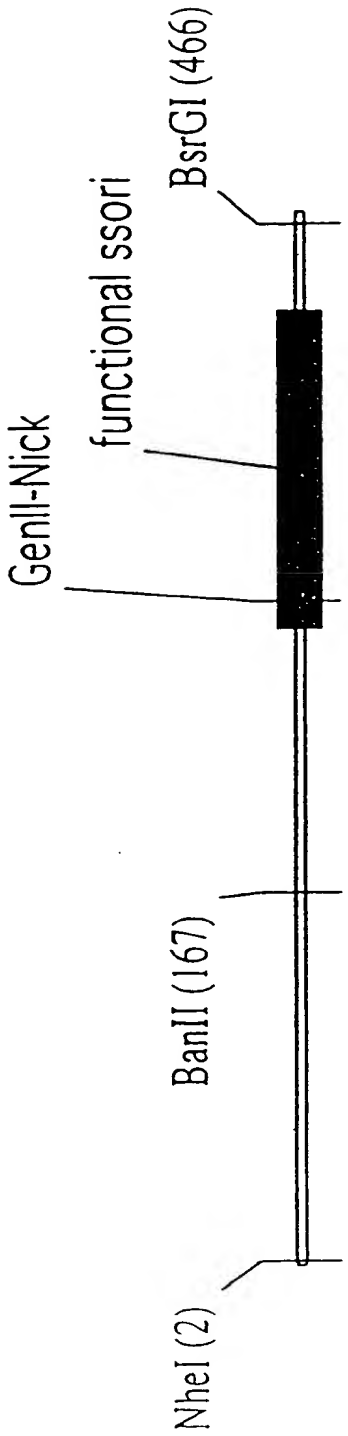
FIG. 35Z

```
701   ACTGGATGGA GGCGGATAAA GTTGCAGGAC CACTTCTGCG CTCGGCCCTT
      TGACCTACCT CCGCCTATTT CAACGTCCTG GTGAAGACGC GAGCCGGGAA

751   CCGGCTGGCT GGTTTATTGC TGATAAATCT GGAGCCGGTG AGCGTGGGTC
      GGCCGACCGA CCAAATAACG ACTATTTAGA CCTCGGCCAC TCGCACCCAG

801   TCGCGGTATC ATTGCAGCAC TGGGGCCAGA TGGTAAGCCC TCCCGTATCG
      AGCGCCATAG TAACGTCGTG ACCCCGGTCT ACCATTCGGG AGGGCATAGC

851   TAGTTATCTA CACGACGGGG AGTCAGGCAA CTATGGATGA ACGAAATAGA
      ATCAATAGAT GTGCTGCCCC TCAGTCCGTT GATACCTACT TGCTTTATCT

901   CAGATCGCTG AGATAGGTGC CTCACTGATT AAGCATTGGG TAACTGTCAG
      GTCTAGCGAC TCTATCCACG GAGTGACTAA TTCGTAACCC ATTGACAGTC

951   ACCAAGTTTA CTCATATATA CTTTAGATTG ATTTAAAACT TCATTTTTAA
      TGGTTCAAAT GAGTATATAT GAAATCTAAC TAAATTTTGA AGTAAAAATT

1001  TTTAAAAGGA TCTAGGTGAA GATCCTTTTT GATAATCTCA TGACCAAAAT
      AAATTTTCCT AGATCCACTT CTAGGAAAAA CTATTAGAGT ACTGGTTTTA

1051  CCCTTAACGT GAGTTTTCGT TCCACTGAGC GTCAGACCCC GTAGAAAAGA
      GGGAATTGCA CTCAAAAGCA AGGTGACTCG CAGTCTGGGG CATCTTTTCT
```

FIG. 35AA

```
                                                        FseI          PacI
                                                      ----------       --
1101  TCAAAGGATC TTCTTGAGAT CCTTTTTGAT AATGGCCGGC CCCCCCCCTT
      AGTTTCCTAG AAGAACTCTA GGAAAAACTA TTACCGGCCG GGGGGGGGAA

      PacI
      ------
1151  AATTAAGGGG GGG
      TTAATTCCCC CCC
```

FIG. 35BB



M11-11
470 bp

FIG. 35CC

M11-II:

```
     NheI
     ~~~~~~
  1  GCTAGCACGC GCCCTGTAGC GGCGCATTAA GCGCGGCGGG TGTGGTGGTT
     CGATCGTGCG CGGGACATCG CCGCGTAATT CGCGCCGCCC ACACCACCAA

 51  ACGCGCAGCG TGACCGCTAC ACTTGCCAGC GCCCTAGCGC CCGCTCCTTT
     TGCGCGTCGC ACTGGCGATG TGAACGGTCG CGGGATCGCG GGCGAGGAAA

101  CGCTTTCTTC CCTTCCTTTC TCGCCACGTT CGCCGGCTTT CCCCGTCAAG
     GCGAAAGAAG GGAAGGAAAG AGCGGTGCAA GCGGCCGAAA GGGGCAGTTC

                  BanII
                  ~~~~~~
151  CTCTAAATCG GGGGCTCCCT TTAGGGTTCC GATTTAGTGC TTTACGGCAC
     GAGATTTAGC CCCCGAGGGA AATCCCAAGG CTAAATCACG AAATGCCGTG

201  CTCGACCCCA AAAAACTTGA TTAGGGTGAT GGTTCTCGTA GTGGGCCATC
     GAGCTGGGGT TTTTTGAACT AATCCCACTA CCAAGAGCAT CACCCGGTAG

251  GCCCTGATAG ACGGTTTTTC GCCCTTTGAC GTTGGAGTCC ACGTTCTTTA
     CGGGACTATC TGCCAAAAAG CGGGAAACTG CAACCTCAGG TGCAAGAAAT
```

FIG. 35DD

```
301   ATAGTGGACT CTTGTTCCAA ACTGGAACAA CACTCAACCC TATCTCGGTC
      TATCACCTGA GAACAAGGTT TGACCTTGTT GTGAGTTGGG ATAGAGCCAG

351   TATTCTTTTG ATTTATAAGG GATTTTGCCG ATTTCGGCCT ATTGGTTAAA
      ATAAGAAAAC TAAATATTCC CTAAAACGGC TAAAGCCGGA TAACCAATTT

401   AAATGAGCTG ATTTAACAAA AATTTAACGC GAATTTTAAC AAAATATTAA
      TTTACTCGAC TAAATTGTTT TTAAATTGCG CTTAAAATTG TTTTATAATT

                        BsrGI
                       ~~~~~~
451   CGTTTACAAT TTCATGTACA
      GCAAATGTTA AAGTACATGT
```

FIG. 35EE

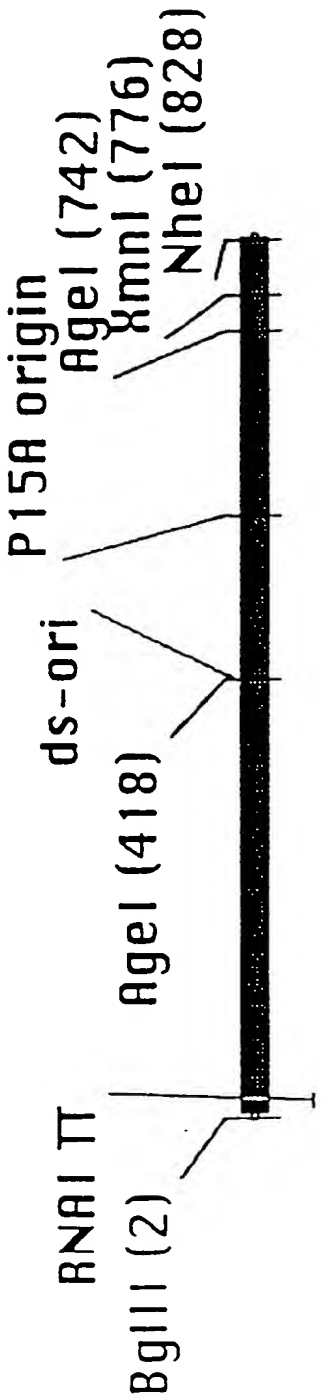

RNAI TT
BglII (2)
AgeI (418)
ds-ori
P15A origin
AgeI (742)
XmnI (776)
NheI (828)
M12
832 bp

FIG. 35FF

M 12:

BglII

~~~~~~

```
  1  AGATCTAATA AGATGATCTT CTTGAGATCG TTTTGGTCTG CGCGTAATCT
     TCTAGATTAT TCTACTAGAA GAACTCTAGC AAAACCAGAC GCGCATTAGA

 51  CTTGCTCTGA AAACGAAAAA ACCGCCTTGC AGGGCGGTTT TTCGTAGGTT
     GAACGAGACT TTTGCTTTTT TGGCGGAACG TCCCGCCAAA AAGCATCCAA

101  CTCTGAGCTA CCAACTCTTT GAACCGAGGT AACTGGCTTG GAGGAGCGCA
     GAGACTCGAT GGTTGAGAAA CTTGGCTCCA TTGACCGAAC CTCCTCGCGT

151  GTCACTAAAA CTTGTCCTTT CAGTTTAGCC TTAACCGGCG CATGACTTCA
     CAGTGATTTT GAACAGGAAA GTCAAATCGG AATTGGCCGC GTACTGAAGT

201  AGACTAACTC CTCTAAATCA ATTACCAGTG GCTGCTGCCA GTGGTGCTTT
     TCTGATTGAG GAGATTTAGT TAATGGTCAC CGACGACGGT CACCACGAAA

251  TGCATGTCTT TCCGGGTTGG ACTCAAGACG ATAGTTACCG GATAAGGCGC
     ACGTACAGAA AGGCCCAACC TGAGTTCTGC TATCAATGGC CTATTCCGCG

301  AGCGGTCGGA CTGAACGGGG GGTTCGTGCA TACAGTCCAG CTTGGAGCGA
     TCGCCAGCCT GACTTGCCCC CCAAGCACGT ATGTCAGGTC GAACCTCGCT
```

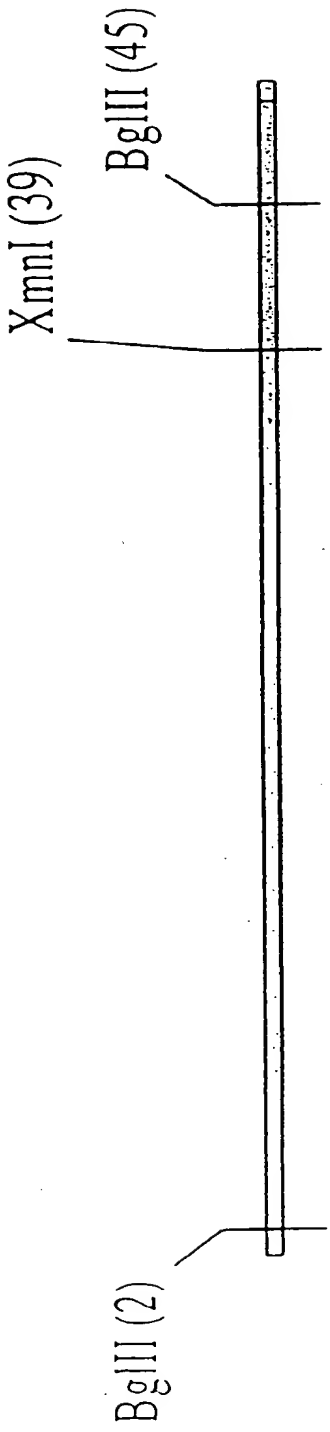
FIG. 35GG
~~~~~~

```
351   ACTGCCTACC CGGAACTGAG TGTCAGGCGT GGAATGAGAC AAACGCGGCC
      TGACGGATGG GCCTTGACTC ACAGTCCGCA CCTTACTCTG TTTGCGCCGG

                            AgeI
                            ~~~~~~~
401   ATAACAGCGG AATGACACCG GTAAACCGAA AGGCAGGAAC AGGAGAGCGC
      TATTGTCGCC TTACTGTGGC CATTTGGCTT TCCGTCCTTG TCCTCTCGCG

451   AGGAGGGAGC CGCCAGGGGG AAACGCCTGG TATCTTTATA GTCCTGTCGG
      TCCTCCCTCG GCGGTCCCCC TTTGCGGACC ATAGAAATAT CAGGACAGCC

501   GTTTCGCCAC CACTGATTTG AGCGTCAGAT TTCGTGATGC TTGTCAGGGG
      CAAAGCGGTG GTGACTAAAC TCGCAGTCTA AAGCACTACG AACAGTCCCC

551   GGCGGAGCCT ATGGAAAAAC GGCTTTGCCG CGGCCCTCTC ACTTCCCTGT
      CCGCCTCGGA TACCTTTTTG CCGAAACGGC GCCGGGAGAG TGAAGGGACA

601   TAAGTATCTT CCTGGCATCT TCCAGGAAAT CTCCGCCCCG TTCGTAAGCC
      ATTCATAGAA GGACCGTAGA AGGTCCTTTA GAGGCGGGGC AAGCATTCGG

651   ATTTCCGCTC GCCGCAGTCG AACGACCGAG CGTAGCGAGT CAGTGAGCGA
      TAAAGGCGAG CGGCGTCAGC TTGCTGGCTC GCATCGCTCA GTCACTCGCT
```

FIG. 35HH

```
                                                          AgeI
                                                          ~~~~~~
701   GGAAGCGGAA TATATCCTGT ATCACATATT CTGCTGACGC ACCGGTGCAG
      CCTTCGCCTT ATATAGGACA TAGTGTATAA GACGACTGCG TGGCCACGTC

                              XmnI
                           ~~~~~~~~~~
751   CCTTTTTTCT CCTGCCACAT GAAGCACTTC ACTGACACCC TCATCAGTGC
      GGAAAAAAGA GGACGGTGTA CTTCGTGAAG TGACTGTGGG AGTAGTCACG

                                    NheI
                                    ~~~~~~
801   CAACATAGTA AGCCAGTATA CACTCCGCTA GC
      GTTGTATCAT TCGGTCATAT GTGAGGCGAT CG
```

FIG. 35II



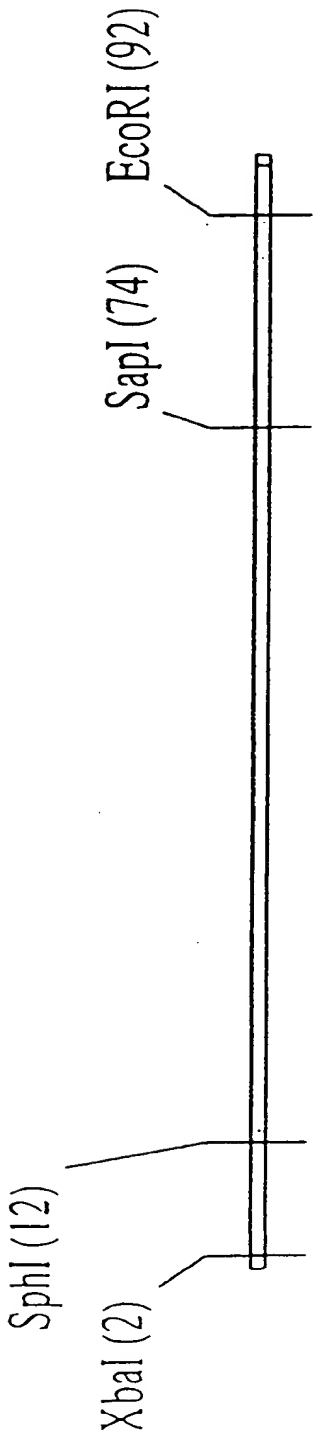
M13
49 bp

FIG. 35JJ

M 13:

```
    BglII                                                XmnI      BglII
    ------                                              ----------------
1   AGATCTCATA ACTTCGTATA ATGTATGCTA TACGAAGTTA TTCAGATCT
    TCTAGAGTAT TGAAGCATAT TACATACGAT ATGCTTCAAT AAGTCTAGA
```

FIG. 35KK



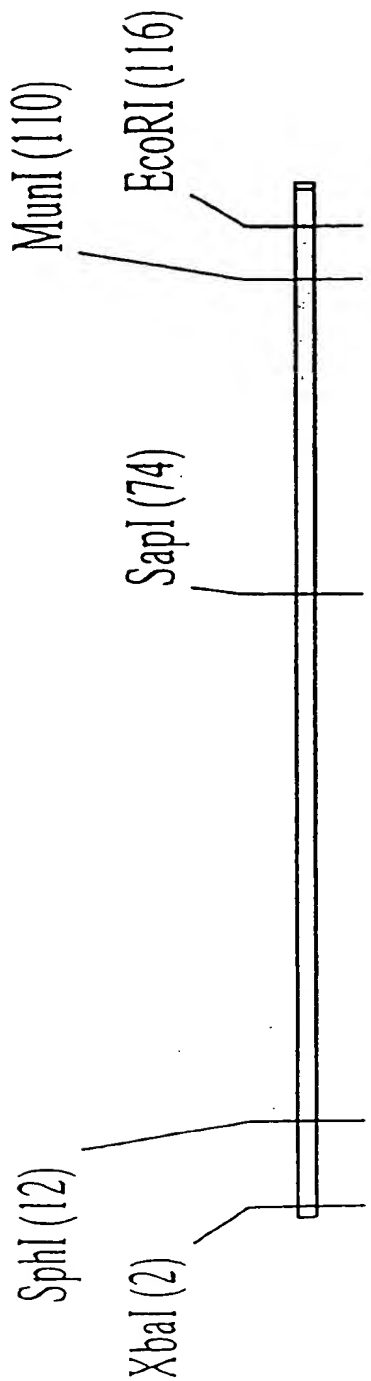
M19
96 bp

FIG. 35LL

M 19:

```
     XbaI  SphI
     ~~~~~~~~~~~~~
 1   TCTAGAGCAT GCGTAGGAGA AAATAAAATG AAACAAAGCA CTATTGCACT
     AGATCTCGTA CGCATCCTCT TTTATTTTAC TTTGTTTCGT GATAACGTGA

                       SapI                          EcoRI
                      ~~~~~~~~                       ~~~~~
51   GGCACTCTTA CCGTTGCTCT TCACCCCTGT TACCAAAGCC GAATTC
     CCGTGAGAAT GGCAACGAGA AGTGGGGACA ATGGTTTCGG CTTAAG
```

FIG. 35MM



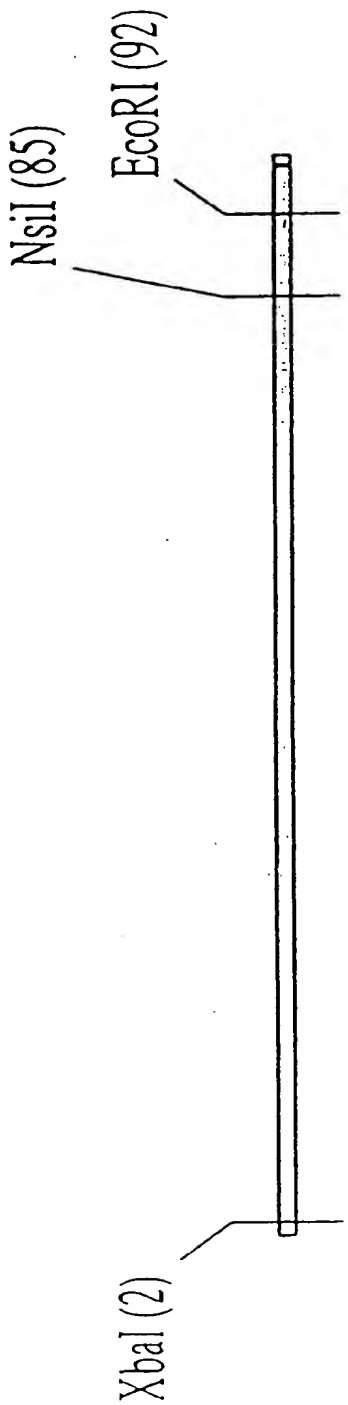
M20
120 bp

FIG. 35NN

M 20:

```
     XbaI  SphI
     ----------
  1  TCTAGAGCAT GCGTAGGAGA AAATAAAATG AAACAAAGCA CTATTGCACT
     AGATCTCGTA CGCATCCTCT TTTATTTTAC TTTGTTTCGT GATAACGTGA

                       SapI
                     ~~~~~~~~
 51  GGCACTCTTA CCGTTGCTCT TCACCCCTGT TACCAAAGCC GACTACAAAG
     CCGTGAGAAT GGCAACGAGA AGTGGGGACA ATGGTTTCGG CTGATGTTTC

               MunI   EcoRI
              ------------
101  ATGAAGTGCA ATTGGAATTC
     TACTTCACGT TAACCTTAAG
```

FIG. 35OO



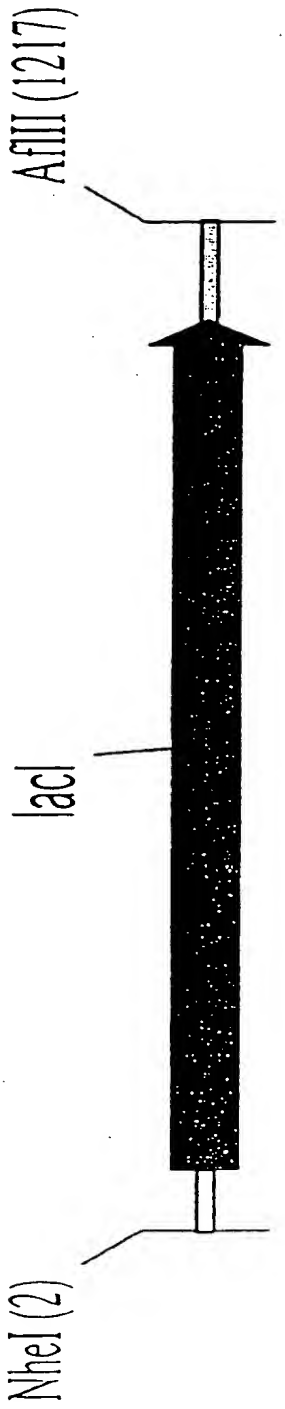
M21
96 bp

FIG. 35PP

M 21:

```
     XbaI
     ------
 1   TCTAGAGGTT GAGGTGATTT TATGAAAAAG AATATCGCAT TTCTTCTTGC
     AGATCTCCAA CTCCACTAAA ATACTTTTTC TTATAGCGTA AAGAAGAACG

                                      NsiI          EcoRI
                                    --------       ------
51   ATCTATGTTC GTTTTTTCTA TTGCTACAAA TGCATACGCT GAATTC
     TAGATACAAG CAAAAAAGAT AACGATGTTT ACGTATGCGA CTTAAG
```

FIG. 35QQ



M41

1221 bp

FIG. 35RR

M 41:

```
     NheI
     ------
  1  GCTAGCATCG AATGGCGCAA AACCTTTCGC GGTATGGCAT GATAGCGCCC
     CGATCGTAGC TTACCGCGTT TTGGAAAGCG CCATACCGTA CTATCGCGGG

 51  GGAAGAGAGT CAATTCAGGG TGGTGAATGT GAAACCAGTA ACGTTATACG
     CCTTCTCTCA GTTAAGTCCC ACCACTTACA CTTTGGTCAT TGCAATATGC

101  ATGTCGCAGA GTATGCCGGT GTCTCTTATC AGACCGTTTC CCGCGTGGTG
     TACAGCGTCT CATACGGCCA CAGAGAATAG TCTGGCAAAG GGCGCACCAC

151  AACCAGGCCA GCCACGTTTC TGCGAAAACG CGGGAAAAAG TGGAAGCGGC
     TTGGTCCGGT CGGTGCAAAG ACGCTTTTGC GCCCTTTTTC ACCTTCGCCG

201  GATGGCGGAG CTGAATTACA TTCCTAACCG CGTGGCACAA CAACTGGCGG
     CTACCGCCTC GACTTAATGT AAGGATTGGC GCACCGTGTT GTTGACCGCC

251  GCAAACAGTC GTTGCTGATT GGCGTTGCCA CCTCCAGTCT GGCCCTGCAC
     CGTTTGTCAG CAACGACTAA CCGCAACGGT GGAGGTCAGA CCGGGACGTG

301  GCGCCGTCGC AAATTGTCGC GGCGATTAAA TCTCGCGCCG ATCAACTGGG
     CGCGGCAGCG TTTAACAGCG CCGCTAATTT AGAGCGCGGC TAGTTGACCC
```

FIG. 35SS

```
351  TGCCAGCGTG GTCGTGTCGA TGGTAGAACG AAGCGGCGTC GAAGCCTGTA
     ACGGTCGCAC CAGCACAGCT ACCATCTTGC TTCGCCGCAG CTTCGGACAT

401  AAGCGGCGGT GCACAATCTT CTCGCGCAAC GTGTCAGTGG GCTGATTATT
     TTCGCCGCCA CGTGTTAGAA GAGCGCGTTG CACAGTCACC CGACTAATAA

451  AACTATCCGC TGGATGACCA GGATGCTATT GCTGTGGAAG CTGCCTGCAC
     TTGATAGGCG ACCTACTGGT CCTACGATAA CGACACCTTC GACGGACGTG

501  TAATGTTCCG GCGTTATTTC TTGATGTCTC TGACCAGACA CCCATCAACA
     ATTACAAGGC CGCAATAAAG AACTACAGAG ACTGGTCTGT GGGTAGTTGT

551  GTATTATTTT CTCCCATGAG GACGGTACGC GACTGGGCGT GGAGCATCTG
     CATAATAAAA GAGGGTACTC CTGCCATGCG CTGACCCGCA CCTCGTAGAC

601  GTCGCATTGG GCCACCAGCA AATCGCGCTG TTAGCTGGCC CATTAAGTTC
     CAGCGTAACC CGGTGGTCGT TTAGCGCGAC AATCGACCGG GTAATTCAAG

651  TGTCTCGGCG CGTCTGCGTC TGGCTGGCTG GCATAAATAT CTCACTCGCA
     ACAGAGCCGC GCAGACGCAG ACCGACCGAC CGTATTTATA GAGTGAGCGT

701  ATCAAATTCA GCCGATAGCG GAACGGGAAG GCGACTGGAG TGCCATGTCC
     TAGTTTAAGT CGGCTATCGC CTTGCCCTTC CGCTGACCTC ACGGTACAGG
```

FIG. 35TT

```
751   GGTTTTCAAC AAACCATGCA AATGCTGAAT GAGGGCATCG TTCCCACTGC
      CCAAAAGTTG TTTGGTACGT TTACGACTTA CTCCCGTAGC AAGGGTGACG

801   GATGCTGGTT GCCAACGATC AGATGGCGCT GGGCGCAATG CGTGCCATTA
      CTACGACCAA CGGTTGCTAG TCTACCGCGA CCCGCGTTAC GCACGGTAAT

851   CCGAGTCCGG GCTGCGCGTT GGTGCGGACA TCTCGGTAGT GGGATACGAC
      GGCTCAGGCC CGACGCGCAA CCACGCCTGT AGAGCCATCA CCCTATGCTG

901   GATACCGAGG ACAGCTCATG TTATATCCCG CCGCTGACCA CCATCAAACA
      CTATGGCTCC TGTCGAGTAC AATATAGGGC GGCGACTGGT GGTAGTTTGT

951   GGATTTTCGC CTGCTGGGGC AAACCAGCGT GGACCGCTTG CTGCAACTCT
      CCTAAAAGCG GACGACCCCG TTTGGTCGCA CCTGGCGAAC GACGTTGAGA

1001  CTCAGGGCCA GGCGGTGAAG GGCAATCAGC TGTTGCCCGT CTCACTGGTG
      GAGTCCCGGT CCGCCACTTC CCGTTAGTCG ACAACGGGCA GAGTGACCAC

1051  AAAAGAAAAA CCACCCTGGC TCCCAATACG CAAACCGCCT CTCCCCGCGC
      TTTTCTTTTT GGTGGGACCG AGGGTTATGC GTTTGGCGGA GAGGGGCGCG

1101  GTTGGCCGAT TCACTGATGC AGCTGGCACG ACAGGTTTCC CGACTGGAAA
      CAACCGGCTA AGTGACTACG TCGACCGTGC TGTCCAAAGG GCTGACCTTT
```

FIG. 35UU

```
1151  GCGGGCAGTG AGGCTACCCG ATAAAAGCGG CTTCCTGACA GGAGGCCGTT
      CGCCCGTCAC TCCGATGGGC TATTTTCGCC GAAGGACTGT CCTCCGGCAA

                          AflII
                          ~~~~~~
1201  TTGTTTTGCA GCCCACTTAA G
      AACAAAACGT CGGGTGAATT C
```

FIG. 35VV

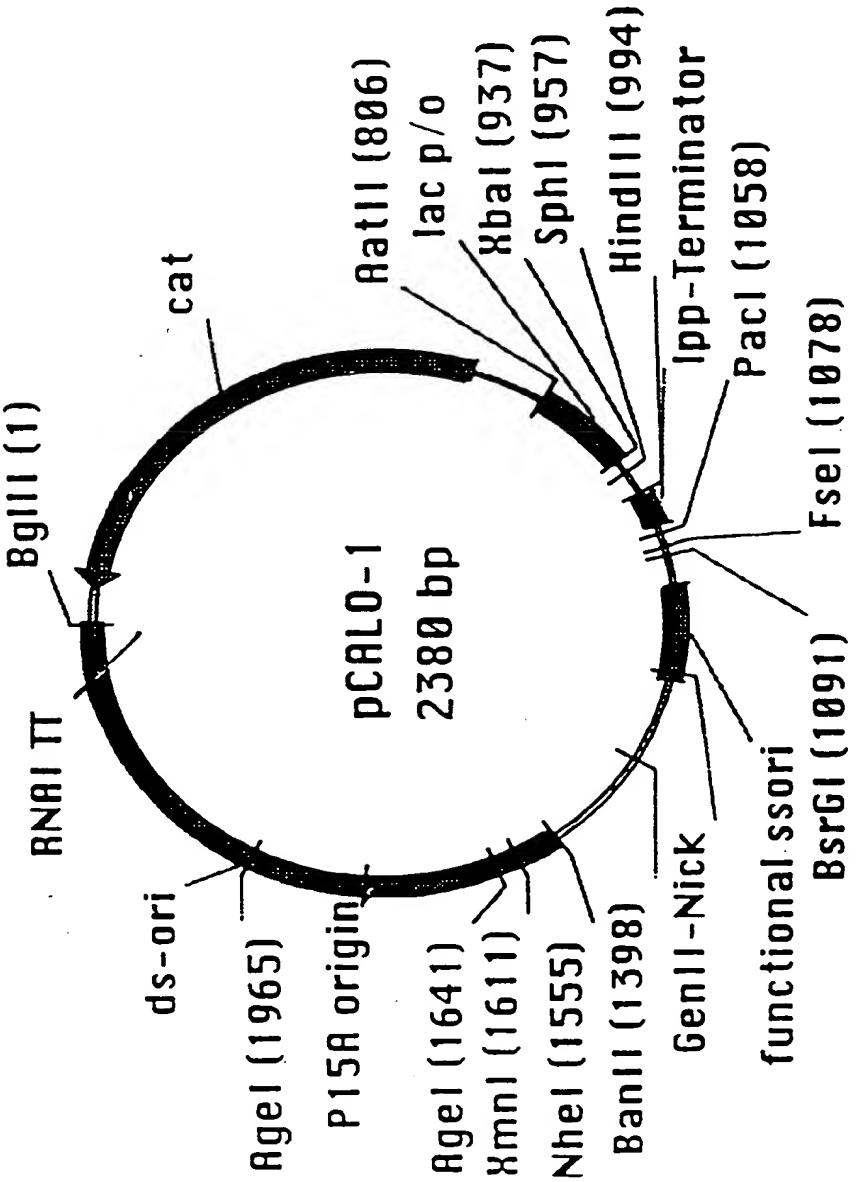

pCALO-1
2380 bp
BglII (1)
cat
AatII (806)
lac p/o
XbaI (937)
SphI (957)
HindIII (994)
lpp-Terminator
PacI (1058)
FseI (1078)
BsrGI (1091)
functional ssori
GenII-Nick
BanII (1398)
NheI (1555)
XmnI (1611)
AgeI (1641)
P15A origin
AgeI (1965)
ds-ori
RNAI TT

FIG. 35WW

pCALO-1:

BglII

~~~~~

```
  1  GATCTAGCAC CAGGCGTTTA AGGGCACCAA TAACTGCCTT AAAAAAATTA
     CTAGATCGTG GTCCGCAAAT TCCCGTGGTT ATTGACGGAA TTTTTTTAAT

 51  CGCCCCGCCC TGCCACTCAT CGCAGTACTG TTGTAATTCA TTAAGCATTC
     GCGGGGCGGG ACGGTGAGTA GCGTCATGAC AACATTAAGT AATTCGTAAG

101  TGCCGACATG GAAGCCATCA CAAACGGCAT GATGAACCTG AATCGCCAGC
     ACGGCTGTAC CTTCGGTAGT GTTTGCCGTA CTACTTGGAC TTAGCGGTCG

151  GGCATCAGCA CCTTGTCGCC TTGCGTATAA TATTTGCCCA TAGTGAAAAC
     CCGTAGTCGT GGAACAGCGG AACGCATATT ATAAACGGGT ATCACTTTTG

201  GGGGGCGAAG AAGTTGTCCA TATTGGCTAC GTTTAAATCA AAACTGGTGA
     CCCCCGCTTC TTCAACAGGT ATAACCGATG CAAATTTAGT TTTGACCACT

251  AACTCACCCA GGGATTGGCT GAGACGAAAA ACATATTCTC AATAAACCCT
     TTGAGTGGGT CCCTAACCGA CTCTGCTTTT TGTATAAGAG TTATTTGGGA

301  TTAGGGAAAT AGGCCAGGTT TTCACCGTAA CACGCCACAT CTTGCGAATA
     AATCCCTTTA TCCGGTCCAA AAGTGGCATT GTGCGGTGTA GAACGCTTAT
```

FIG. 35XX
~~~~~

```
351  TATGTGTAGA AACTGCCGGA AATCGTCGTG GTATTCACTC CAGAGCGATG
     ATACACATCT TTGACGGCCT TTAGCAGCAC CATAAGTGAG GTCTCGCTAC

401  AAAACGTTTC AGTTTGCTCA TGGAAAACGG TGTAACAAGG GTGAACACTA
     TTTTGCAAAG TCAAACGAGT ACCTTTTGCC ACATTGTTCC CACTTGTGAT

451  TCCCATATCA CCAGCTCACC GTCTTTCATT GCCATACGGA ACTCCGGGTG
     AGGGTATAGT GGTCGAGTGG CAGAAAGTAA CGGTATGCCT TGAGGCCCAC

501  AGCATTCATC AGGCGGGCAA GAATGTGAAT AAAGGCCGGA TAAAACTTGT
     TCGTAAGTAG TCCGCCCGTT CTTACACTTA TTTCCGGCCT ATTTTGAACA

551  GCTTATTTTT CTTTACGGTC TTTAAAAAGG CCGTAATATC CAGCTGAACG
     CGAATAAAAA GAAATGCCAG AAATTTTTCC GGCATTATAG GTCGACTTGC

601  GTCTGGTTAT AGGTACATTG AGCAACTGAC TGAAATGCCT CAAAATGTTC
     CAGACCAATA TCCATGTAAC TCGTTGACTG ACTTTACGGA GTTTTACAAG

651  TTTACGATGC CATTGGGATA TATCAACGGT GGTATATCCA GTGATTTTTT
     AAATGCTACG GTAACCCTAT ATAGTTGCCA CCATATAGGT CACTAAAAAA

701  TCTCCATTTT AGCTTCCTTA GCTCCTGAAA ATCTCGATAA CTCAAAAAAT
     AGAGGTAAAA TCGAAGGAAT CGAGGACTTT TAGAGCTATT GAGTTTTTTA
```

FIG. 35YY

```
751   ACGCCCGGTA GTGATCTTAT TTCATTATGG TGAAAGTTGG AACCTCACCC
      TGCGGGCCAT CACTAGAATA AAGTAATACC ACTTTCAACC TTGGAGTGGG

       AatII
      ~~~~~~
801   GACGTCTAAT GTGAGTTAGC TCACTCATTA GGCACCCCAG GCTTTACACT
      CTGCAGATTA CACTCAATCG AGTGAGTAAT CCGTGGGGTC CGAAATGTGA

851   TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG ATAACAATTT
      AATACGAAGG CCGAGCATAC AACACACCTT AACACTCGCC TATTGTTAAA

                                              XbaI
                                             ~~~~~~~
901   CACACAGGAA ACAGCTATGA CCATGATTAC GAATTTCTAG ACCCCCCCCC
      GTGTGTCCTT TGTCGATACT GGTACTAATG CTTAAAGATC TGGGGGGGGG

        SphI                                          HindIII
       ~~~~~~                                        ~~~~~~
951   CGCATGCCAT AACTTCGTAT AATGTACGCT ATACGAAGTT ATAAGCTTGA
      GCGTACGGTA TTGAAGCATA TTACATGCGA TATGCTTCAA TATTCGAACT

1001  CCTGTGAAGT GAAAAATGGC GCAGATTGTG CGACATTTTT TTTGTCTGCC
      GGACACTTCA CTTTTTACCG CGTCTAACAC GCTGTAAAAA AAACAGACGG
```

FIG. 35ZZ

```
          PacI                    FseI                    BsrGI
          ~~~~~~~~                ~~~~~~~~                ~~~~~~~
1051  GTTTAATTAA AGGGGGGGGG GGGCCGGCCT GGGGGGGGGT GTACATGAAA
      CAAATTAATT TCCCCCCCCC CCCGGCCGGA CCCCCCCCCA CATGTACTTT

1101  TTGTAAACGT TAATATTTTG TTAAAATTCG CGTTAAATTT TTGTTAAATC
      AACATTTGCA ATTATAAAAC AATTTTAAGC GCAATTTAAA AACAATTTAG

1151  AGCTCATTTT TTAACCAATA GGCCGAAATC GGCAAAATCC CTTATAAATC
      TCGAGTAAAA AATTGGTTAT CCGGCTTTAG CCGTTTTAGG GAATATTTAG

1201  AAAAGAATAG ACCGAGATAG GGTTGAGTGT TGTTCCAGTT TGGAACAAGA
      TTTTCTTATC TGGCTCTATC CCAACTCACA ACAAGGTCAA ACCTTGTTCT

1251  GTCCACTATT AAAGAACGTG GACTCCAACG TCAAAGGGCG AAAAACCGTC
      CAGGTGATAA TTTCTTGCAC CTGAGGTTGC AGTTTCCCGC TTTTTGGCAG

1301  TATCAGGGCG ATGGCCCACT ACGAGAACCA TCACCCTAAT CAAGTTTTTT
      ATAGTCCCGC TACCGGGTGA TGCTCTTGGT AGTGGGATTA GTTCAAAAAA

                                                    BanII
                                                    ~~~~~~
1351  GGGGTCGAGG TGCCGTAAAG CACTAAATCG GAACCCTAAA GGGAGCCCCC
      CCCCAGCTCC ACGGCATTTC GTGATTTAGC CTTGGGATTT CCCTCGGGGG
```

FIG. 35AAA

```
1401  GATTTAGAGC TTGACGGGGA AAGCCGGCGA ACGTGGCGAG AAAGGAAGGG
      CTAAATCTCG AACTGCCCCT TTCGGCCGCT TGCACCGCTC TTTCCTTCCC

1451  AAGAAAGCGA AAGGAGCGGG CGCTAGGGCG CTGGCAAGTG TAGCGGTCAC
      TTCTTTCGCT TTCCTCGCCC GCGATCCCGC GACCGTTCAC ATCGCCAGTG

1501  GCTGCGCGTA ACCACCACAC CCGCCGCGCT TAATGCGCCG CTACAGGGCG
      CGACGCGCAT TGGTGGTGTG GGCGGCGCGA ATTACGCGGC GATGTCCCGC

          NheI
        ~~~~~~
1551  CGTGCTAGCG GAGTGTATAC TGGCTTACTA TGTTGGCACT GATGAGGGTG
      GCACGATCGC CTCACATATG ACCGAATGAT ACAACCGTGA CTACTCCCAC

              XmnI                                    AgeI
          ~~~~~~~~~~~                              ~~~~~~~
1601  TCAGTGAAGT GCTTCATGTG GCAGGAGAAA AAAGGCTGCA CCGGTGCGTC
      AGTCACTTCA CGAAGTACAC CGTCCTCTTT TTTCCGACGT GGCCACGCAG

1651  AGCAGAATAT GTGATACAGG ATATATTCCG CTTCCTCGCT CACTGACTCG
      TCGTCTTATA CACTATGTCC TATATAAGGC GAAGGAGCGA GTGACTGAGC

1701  CTACGCTCGG TCGTTCGACT GCGGCGAGCG GAAATGGCTT ACGAACGGGG
```

FIG. 35BBB

```
        GATGCGAGCC AGCAAGCTGA CGCCGCTCGC CTTTACCGAA TGCTTGCCCC

1751    CGGAGATTTC CTGGAAGATG CCAGGAAGAT ACTTAACAGG GAAGTGAGAG
        GCCTCTAAAG GACCTTCTAC GGTCCTTCTA TGAATTGTCC CTTCACTCTC

1801    GGCCGCGGCA AAGCCGTTTT TCCATAGGCT CCGCCCCCCT GACAAGCATC
        CCGGCGCCGT TTCGGCAAAA AGGTATCCGA GGCGGGGGGA CTGTTCGTAG

1851    ACGAAATCTG ACGCTCAAAT CAGTGGTGGC GAAACCCGAC AGGACTATAA
        TGCTTTAGAC TGCGAGTTTA GTCACCACCG CTTTGGGCTG TCCTGATATT

1901    AGATACCAGG CGTTTCCCCC TGGCGGCTCC CTCCTGCGCT CTCCTGTTCC
        TCTATGGTCC GCAAAGGGGG ACCGCCGAGG GAGGACGCGA GAGGACAAGG

                        AgeI
                        ~~~~~~
1951    TGCCTTTCGG TTTACCGGTG TCATTCCGCT GTTATGGCCG CGTTTGTCTC
        ACGGAAAGCC AAATGGCCAC AGTAAGGCGA CAATACCGGC GCAAACAGAG

2001    ATTCCACGCC TGACACTCAG TTCCGGGTAG GCAGTTCGCT CCAAGCTGGA
        TAAGGTGCGG ACTGTGAGTC AAGGCCCATC CGTCAAGCGA GGTTCGACCT

2051    CTGTATGCAC GAACCCCCCG TTCAGTCCGA CCGCTGCGCC TTATCCGGTA
        GACATACGTG CTTGGGGGGC AAGTCAGGCT GGCGACGCGG AATAGGCCAT
```

FIG. 35CCC

```
2101   ACTATCGTCT TGAGTCCAAC CCGGAAAGAC ATGCAAAAGC ACCACTGGCA
       TGATAGCAGA ACTCAGGTTG GGCCTTTCTG TACGTTTTCG TGGTGACCGT

2151   GCAGCCACTG GTAATTGATT TAGAGGAGTT AGTCTTGAAG TCATGCGCCG
       CGTCGGTGAC CATTAACTAA ATCTCCTCAA TCAGAACTTC AGTACGCGGC

2201   GTTAAGGCTA AACTGAAAGG ACAAGTTTTA GTGACTGCGC TCCTCCAAGC
       CAATTCCGAT TTGACTTTCC TGTTCAAAAT CACTGACGCG AGGAGGTTCG

2251   CAGTTACCTC GGTTCAAAGA GTTGGTAGCT CAGAGAACCT ACGAAAAACC
       GTCAATGGAG CCAAGTTTCT CAACCATCGA GTCTCTTGGA TGCTTTTTGG

2301   GCCCTGCAAG GCGGTTTTTT CGTTTTCAGA GCAAGAGATT ACGCGCAGAC
       CGGGACGTTC CGCCAAAAAA GCAAAAGTCT CGTTCTCTAA TGCGCGTCTG

                                                  BglII
                                                    ~
2351   CAAAACGATC TCAAGAAGAT CATCTTATTA
       GTTTTGCTAG AGTTCTTCTA GTAGAATAAT
```

FIG. 35DDD

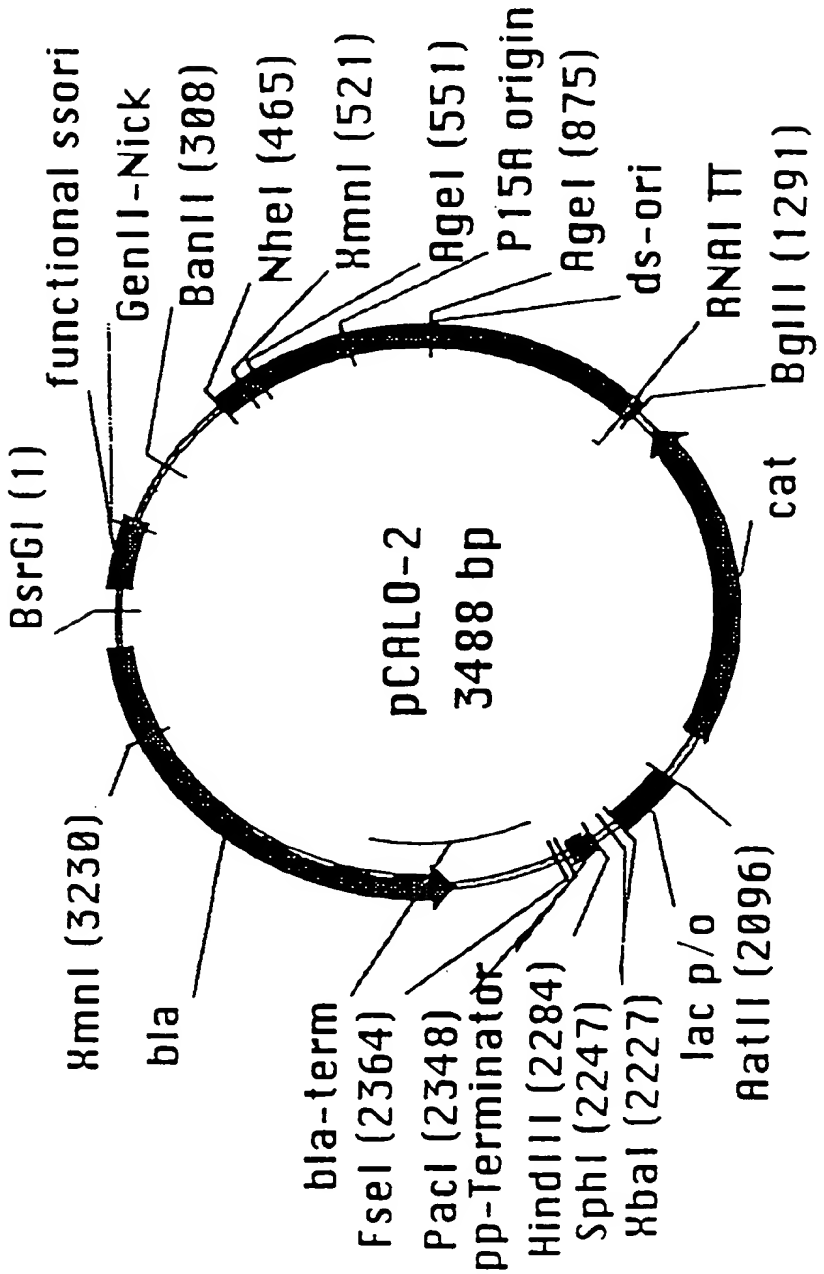

pCALO-2
3488 bp
BsrGI (1)
functional ssori
GenII-Nick
BanII (308)
NheI (465)
XmnI (521)
AgeI (551)
P15A origin
AgeI (875)
ds-ori
RNAI TT
BglII (1291)
cat
AatII (2096)
lac p/o
XbaI (2227)
SphI (2247)
HindIII (2284)
lpp-Terminator
PacI (2348)
FseI (2364)
bla-term
bla
XmnI (3230)

FIG. 35EEE

pCALO-2:

BsrGI

~~~~~

```
  1  GTACATGAAA TTGTAAACGT TAATATTTTG TTAAAATTCG CGTTAAATTT
     CATGTACTTT AACATTTGCA ATTATAAAAC AATTTTAAGC GCAATTTAAA

 51  TTGTTAAATC AGCTCATTTT TTAACCAATA GGCCGAAATC GGCAAAATCC
     AACAATTTAG TCGAGTAAAA AATTGGTTAT CCGGCTTTAG CCGTTTTAGG

101  CTTATAAATC AAAAGAATAG ACCGAGATAG GGTTGAGTGT TGTTCCAGTT
     GAATATTTAG TTTTCTTATC TGGCTCTATC CCAACTCACA ACAAGGTCAA

151  TGGAACAAGA GTCCACTATT AAAGAACGTG GACTCCAACG TCAAAGGGCG
     ACCTTGTTCT CAGGTGATAA TTTCTTGCAC CTGAGGTTGC AGTTTCCCGC

201  AAAAACCGTC TATCAGGGCG ATGGCCCACT ACGAGAACCA TCACCCTAAT
     TTTTTGGCAG ATAGTCCCGC TACCGGGTGA TGCTCTTGGT AGTGGGATTA

251  CAAGTTTTTT GGGGTCGAGG TGCCGTAAAG CACTAAATCG GAACCCTAAA
     GTTCAAAAAA CCCCAGCTCC ACGGCATTTC GTGATTTAGC CTTGGGATTT
```

BanII

~~~~~~

```
301  GGGAGCCCCC GATTTAGAGC TTGACGGGGA AAGCCGGCGA ACGTGGCGAG
```

FIG. 35FFF

```
      CCCTCGGGGG CTAAATCTCG AACTGCCCCT TTCGGCCGCT TGCACCGCTC

351   AAAGGAAGGG AAGAAAGCGA AAGGAGCGGG CGCTAGGGCG CTGGCAAGTG
      TTTCCTTCCC TTCTTTCGCT TTCCTCGCCC GCGATCCCGC GACCGTTCAC

401   TAGCGGTCAC GCTGCGCGTA ACCACCACAC CCGCCGCGCT TAATGCGCCG
      ATCGCCAGTG CGACGCGCAT TGGTGGTGTG GGCGGCGCGA ATTACGCGGC

                       NheI
                      ~~~~~~
451   CTACAGGGCG CGTGCTAGCG GAGTGTATAC TGGCTTACTA TGTTGGCACT
      GATGTCCCGC GCACGATCGC CTCACATATG ACCGAATGAT ACAACCGTGA

                          XmnI                              AgeI
                        ~~~~~~~~~~~                          ~
501   GATGAGGGTG TCAGTGAAGT GCTTCATGTG GCAGGAGAAA AAAGGCTGCA
      CTACTCCCAC AGTCACTTCA CGAAGTACAC CGTCCTCTTT TTTCCGACGT

      AgeI
      ~~~~~
551   CCGGTGCGTC AGCAGAATAT GTGATACAGG ATATATTCCG CTTCCTCGCT
      GGCCACGCAG TCGTCTTATA CACTATGTCC TATATAAGGC GAAGGAGCGA

601   CACTGACTCG CTACGCTCGG TCGTTCGACT GCGGCGAGCG GAAATGGCTT
```

FIG. 35GGG

```
       GTGACTGAGC GATGCGAGCC AGCAAGCTGA CGCCGCTCGC CTTTACCGAA

651    ACGAACGGGG CGGAGATTTC CTGGAAGATG CCAGGAAGAT ACTTAACAGG
       TGCTTGCCCC GCCTCTAAAG GACCTTCTAC GGTCCTTCTA TGAATTGTCC

701    GAAGTGAGAG GGCCGCGGCA AAGCCGTTTT TCCATAGGCT CCGCCCCCCT
       CTTCACTCTC CCGGCGCCGT TTCGGCAAAA AGGTATCCGA GGCGGGGGGA

751    GACAAGCATC ACGAAATCTG ACGCTCAAAT CAGTGGTGGC GAAACCCGAC
       CTGTTCGTAG TGCTTTAGAC TGCGAGTTTA GTCACCACCG CTTTGGGCTG

801    AGGACTATAA AGATACCAGG CGTTTCCCCC TGGCGGCTCC CTCCTGCGCT
       TCCTGATATT TCTATGGTCC GCAAAGGGGG ACCGCCGAGG GAGGACGCGA

                                  AgeI
                                  ~~~~~~
851    CTCCTGTTCC TGCCTTTCGG TTTACCGGTG TCATTCCGCT GTTATGGCCG
       GAGGACAAGG ACGGAAAGCC AAATGGCCAC AGTAAGGCGA CAATACCGGC

901    CGTTTGTCTC ATTCCACGCC TGACACTCAG TTCCGGGTAG GCAGTTCGCT
       GCAAACAGAG TAAGGTGCGG ACTGTGAGTC AAGGCCCATC CGTCAAGCGA

951    CCAAGCTGGA CTGTATGCAC GAACCCCCCG TTCAGTCCGA CCGCTGCGCC
       GGTTCGACCT GACATACGTG CTTGGGGGGC AAGTCAGGCT GGCGACGCGG
```

FIG. 35HHH

```
1001   TTATCCGGTA ACTATCGTCT TGAGTCCAAC CCGGAAAGAC ATGCAAAAGC
       AATAGGCCAT TGATAGCAGA ACTCAGGTTG GGCCTTTCTG TACGTTTTCG

1051   ACCACTGGCA GCAGCCACTG GTAATTGATT TAGAGGAGTT AGTCTTGAAG
       TGGTGACCGT CGTCGGTGAC CATTAACTAA ATCTCCTCAA TCAGAACTTC

1101   TCATGCGCCG GTTAAGGCTA AACTGAAAGG ACAAGTTTTA GTGACTGCGC
       AGTACGCGGC CAATTCCGAT TTGACTTTCC TGTTCAAAAT CACTGACGCG

1151   TCCTCCAAGC CAGTTACCTC GGTTCAAAGA GTTGGTAGCT CAGAGAACCT
       AGGAGGTTCG GTCAATGGAG CCAAGTTTCT CAACCATCGA GTCTCTTGGA

1201   ACGAAAAACC GCCCTGCAAG GCGGTTTTTT CGTTTTCAGA GCAAGAGATT
       TGCTTTTTGG CGGGACGTTC CGCCAAAAAA GCAAAAGTCT CGTTCTCTAA

                                                    BglII
                                                  ~~~~~~~
1251   ACGCGCAGAC CAAAACGATC TCAAGAAGAT CATCTTATTA GATCTAGCAC
       TGCGCGTCTG GTTTTGCTAG AGTTCTTCTA GTAGAATAAT CTAGATCGTG

1301   CAGGCGTTTA AGGGCACCAA TAACTGCCTT AAAAAAATTA CGCCCCGCCC
       GTCCGCAAAT TCCCGTGGTT ATTGACGGAA TTTTTTTAAT GCGGGGCGGG
```

FIG. 35III

```
1351  TGCCACTCAT CGCAGTACTG TTGTAATTCA TTAAGCATTC TGCCGACATG
      ACGGTGAGTA GCGTCATGAC AACATTAAGT AATTCGTAAG ACGGCTGTAC

1401  GAAGCCATCA CAAACGGCAT GATGAACCTG AATCGCCAGC GGCATCAGCA
      CTTCGGTAGT GTTTGCCGTA CTACTTGGAC TTAGCGGTCG CCGTAGTCGT

1451  CCTTGTCGCC TTGCGTATAA TATTTGCCCA TAGTGAAAAC GGGGGCGAAG
      GGAACAGCGG AACGCATATT ATAAACGGGT ATCACTTTTG CCCCCGCTTC

1501  AAGTTGTCCA TATTGGCTAC GTTTAAATCA AAACTGGTGA AACTCACCCA
      TTCAACAGGT ATAACCGATG CAAATTTAGT TTTGACCACT TTGAGTGGGT

1551  GGGATTGGCT GAGACGAAAA ACATATTCTC AATAAACCCT TTAGGGAAAT
      CCCTAACCGA CTCTGCTTTT TGTATAAGAG TTATTTGGGA AATCCCTTTA

1601  AGGCCAGGTT TTCACCGTAA CACGCCACAT CTTGCGAATA TATGTGTAGA
      TCCGGTCCAA AAGTGGCATT GTGCGGTGTA GAACGCTTAT ATACACATCT

1651  AACTGCCGGA AATCGTCGTG GTATTCACTC CAGAGCGATG AAAACGTTTC
      TTGACGGCCT TTAGCAGCAC CATAAGTGAG GTCTCGCTAC TTTTGCAAAG

1701  AGTTTGCTCA TGGAAAACGG TGTAACAAGG GTGAACACTA TCCCATATCA
      TCAAACGAGT ACCTTTTGCC ACATTGTTCC CACTTGTGAT AGGGTATAGT
```

FIG. 35JJJ

```
1751  CCAGCTCACC GTCTTTCATT GCCATACGGA ACTCCGGGTG AGCATTCATC
      GGTCGAGTGG CAGAAAGTAA CGGTATGCCT TGAGGCCCAC TCGTAAGTAG

1801  AGGCGGGCAA GAATGTGAAT AAAGGCCGGA TAAAACTTGT GCTTATTTTT
      TCCGCCCGTT CTTACACTTA TTTCCGGCCT ATTTTGAACA CGAATAAAAA

1851  CTTTACGGTC TTTAAAAAGG CCGTAATATC CAGCTGAACG GTCTGGTTAT
      GAAATGCCAG AAATTTTTCC GGCATTATAG GTCGACTTGC CAGACCAATA

1901  AGGTACATTG AGCAACTGAC TGAAATGCCT CAAAATGTTC TTTACGATGC
      TCCATGTAAC TCGTTGACTG ACTTTACGGA GTTTTACAAG AAATGCTACG

1951  CATTGGGATA TATCAACGGT GGTATATCCA GTGATTTTTT TCTCCATTTT
      GTAACCCTAT ATAGTTGCCA CCATATAGGT CACTAAAAAA AGAGGTAAAA

2001  AGCTTCCTTA GCTCCTGAAA ATCTCGATAA CTCAAAAAAT ACGCCCGGTA
      TCGAAGGAAT CGAGGACTTT TAGAGCTATT GAGTTTTTTA TGCGGGCCAT

                                                   AatII
                                                   ~~~~~~
2051  GTGATCTTAT TTCATTATGG TGAAAGTTGG AACCTCACCC GACGTCTAAT
      CACTAGAATA AAGTAATACC ACTTTCAACC TTGGAGTGGG CTGCAGATTA

2101  GTGAGTTAGC TCACTCATTA GGCACCCCAG GCTTTACACT TTATGCTTCC
```

FIG. 35KKK

```
       CACTCAATCG AGTGAGTAAT CCGTGGGGTC CGAAATGTGA AATACGAAGG

2151   GGCTCGTATG TTGTGTGGAA TTGTGAGCGG ATAACAATTT CACACAGGAA
       CCGAGCATAC AACACACCTT AACACTCGCC TATTGTTAAA GTGTGTCCTT

                                   XbaI                 SphI
                                  ~~~~~~~              ~~~~~~
2201   ACAGCTATGA CCATGATTAC GAATTTCTAG ACCCCCCCCC CGCATGCCAT
       TGTCGATACT GGTACTAATG CTTAAAGATC TGGGGGGGGG GCGTACGGTA

                                            HindIII
                                            ~~~~~~
2251   AACTTCGTAT AATGTACGCT ATACGAAGTT ATAAGCTTGA CCTGTGAAGT
       TTGAAGCATA TTACATGCGA TATGCTTCAA TATTCGAACT GGACACTTCA

                                                     PacI
                                                    ~~~~~~~~
2301   GAAAAATGGC GCAGATTGTG CGACATTTTT TTTGTCTGCC GTTTAATTAA
       CTTTTTACCG CGTCTAACAC GCTGTAAAAA AAACAGACGG CAAATTAATT

                FseI
               ~~~~~~~~~
2351   GGGGGGGGGC CGGCCATTAT CAAAAAGGAT CTCAAGAAGA TCCTTTGATC
       CCCCCCCCCG GCCGGTAATA GTTTTTCCTA GAGTTCTTCT AGGAAACTAG
```

FIG. 35LLL

```
2401   TTTTCTACGG GGTCTGACGC TCAGTGGAAC GAAAACTCAC GTTAAGGGAT
       AAAAGATGCC CCAGACTGCG AGTCACCTTG CTTTTGAGTG CAATTCCCTA

2451   TTTGGTCATG AGATTATCAA AAAGGATCTT CACCTAGATC CTTTTAAATT
       AAACCAGTAC TCTAATAGTT TTTCCTAGAA GTGGATCTAG GAAAATTTAA

2501   AAAAATGAAG TTTTAAATCA ATCTAAAGTA TATATGAGTA AACTTGGTCT
       TTTTTACTTC AAAATTTAGT TAGATTTCAT ATATACTCAT TTGAACCAGA

2551   GACAGTTACC CAATGCTTAA TCAGTGAGGC ACCTATCTCA GCGATCTGTC
       CTGTCAATGG GTTACGAATT AGTCACTCCG TGGATAGAGT CGCTAGACAG

2601   TATTTCGTTC ATCCATAGTT GCCTGACTCC CCGTCGTGTA GATAACTACG
       ATAAAGCAAG TAGGTATCAA CGGACTGAGG GGCAGCACAT CTATTGATGC

2651   ATACGGGAGG GCTTACCATC TGGCCCCAGT GCTGCAATGA TACCGCGAGA
       TATGCCCTCC CGAATGGTAG ACCGGGGTCA CGACGTTACT ATGGCGCTCT

2701   CCCACGCTCA CCGGCTCCAG ATTTATCAGC AATAAACCAG CCAGCCGGAA
       GGGTGCGAGT GGCCGAGGTC TAAATAGTCG TTATTTGGTC GGTCGGCCTT

2751   GGGCCGAGCG CAGAAGTGGT CCTGCAACTT TATCCGCCTC CATCCAGTCT
       CCCGGCTCGC GTCTTCACCA GGACGTTGAA ATAGGCGGAG GTAGGTCAGA
```

FIG. 35MMM

```
2801  ATTAACTGTT GCCGGGAAGC TAGAGTAAGT AGTTCGCCAG TTAATAGTTT
      TAATTGACAA CGGCCCTTCG ATCTCATTCA TCAAGCGGTC AATTATCAAA

2851  GCGCAACGTT GTTGCCATTG CTACAGGCAT CGTGGTGTCA CGCTCGTCGT
      CGCGTTGCAA CAACGGTAAC GATGTCCGTA GCACCACAGT GCGAGCAGCA

2901  TTGGTATGGC TTCATTCAGC TCCGGTTCCC AACGATCAAG GCGAGTTACA
      AACCATACCG AAGTAAGTCG AGGCCAAGGG TTGCTAGTTC CGCTCAATGT

2951  TGATCCCCCA TGTTGTGCAA AAAAGCGGTT AGCTCCTTCG GTCCTCCGAT
      ACTAGGGGGT ACAACACGTT TTTTCGCCAA TCGAGGAAGC CAGGAGGCTA

3001  CGTTGTCAGA AGTAAGTTGG CCGCAGTGTT ATCACTCATG GTTATGGCAG
      GCAACAGTCT TCATTCAACC GGCGTCACAA TAGTGAGTAC CAATACCGTC

3051  CACTGCATAA TTCTCTTACT GTCATGCCAT CCGTAAGATG CTTTTCTGTG
      GTGACGTATT AAGAGAATGA CAGTACGGTA GGCATTCTAC GAAAAGACAC

3101  ACTGGTGAGT ACTCAACCAA GTCATTCTGA GAATAGTGTA TGCGGCGACC
      TGACCACTCA TGAGTTGGTT CAGTAAGACT CTTATCACAT ACGCCGCTGG

3151  GAGTTGCTCT TGCCCGGCGT CAATACGGGA TAATACCGCG CCACATAGCA
      CTCAACGAGA ACGGGCCGCA GTTATGCCCT ATTATGGCGC GGTGTATCGT
```

FIG. 35NNN

```
                                        XmnI
                                        ~~~~~~~~~~~
3201  GAACTTTAAA AGTGCTCATC ATTGGAAAAC GTTCTTCGGG GCGAAAACTC
      CTTGAAATTT TCACGAGTAG TAACCTTTTG CAAGAAGCCC CGCTTTTGAG

3251  TCAAGGATCT TACCGCTGTT GAGATCCAGT TCGATGTAAC CCACTCGCGC
      AGTTCCTAGA ATGGCGACAA CTCTAGGTCA AGCTACATTG GGTGAGCGCG

3301  ACCCAACTGA TCCTCAGCAT CTTTTACTTT CACCAGCGTT TCTGGGTGAG
      TGGGTTGACT AGGAGTCGTA GAAAATGAAA GTGGTCGCAA AGACCCACTC

3351  CAAAAACAGG AAGGCAAAAT GCCGCAAAAA AGGGAATAAG GGCGACACGG
      GTTTTTGTCC TTCCGTTTTA CGGCGTTTTT TCCCTTATTC CCGCTGTGCC

3401  AAATGTTGAA TACTCATACT CTTCCTTTTT CAATATTATT GAAGCATTTA
      TTTACAACTT ATGAGTATGA GAAGGAAAAA GTTATAATAA CTTCGTAAAT

                                              BsrGI

3451  TCAGGGTTAT TGTCTCATGA GCGGATACAT ATTTGAAT
      AGTCCCAATA ACAGAGTACT CGCCTATGTA TAAACTTA
```

FIG. 35OO

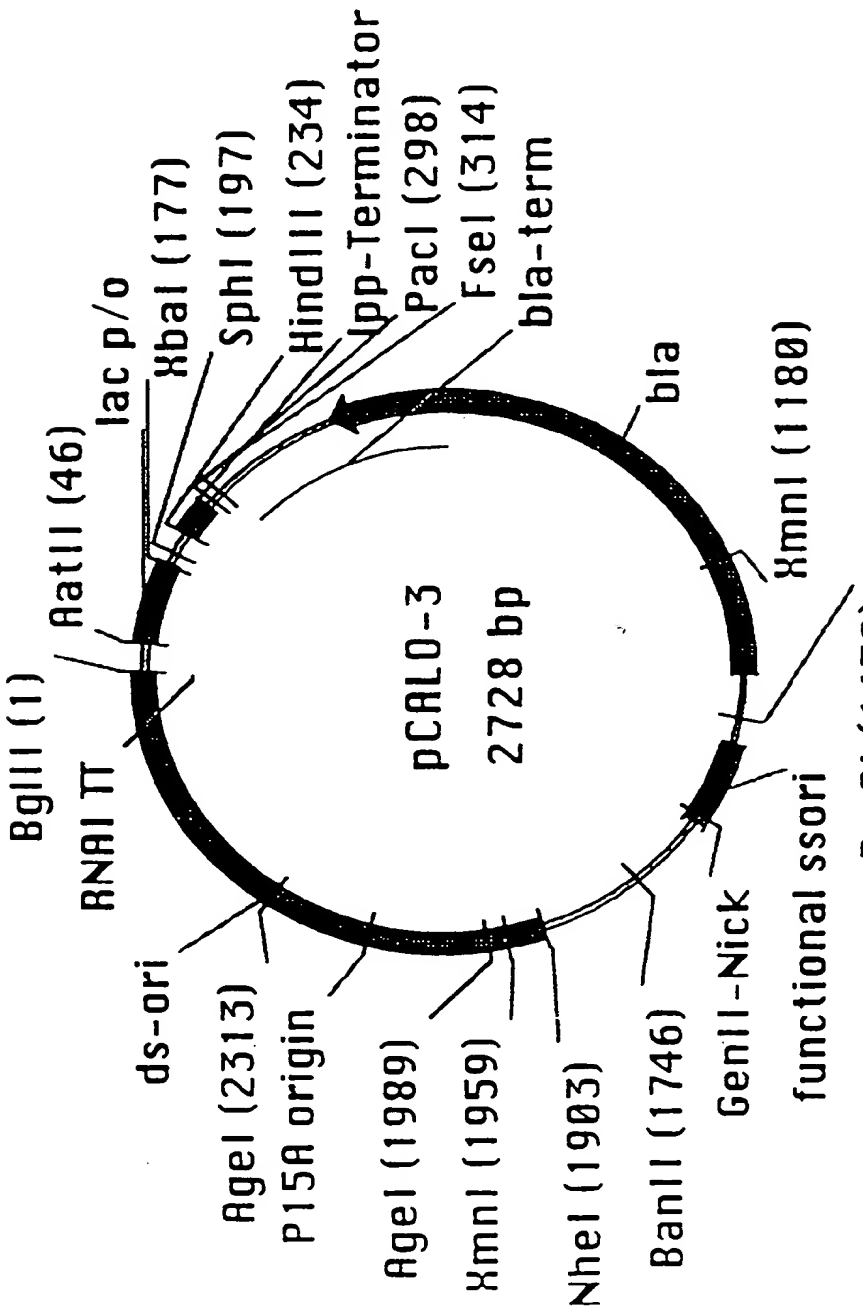

pCAL0-3
2728 bp
BglII (1)
RNAI TT
AatII (46)
lac p/o
XbaI (177)
SphI (197)
HindIII (234)
lpp-Terminator
PacI (298)
FseI (314)
bla-term
bla
XmnI (1180)
BsrGI (1439)
functional ssori
GenII-Nick
BanII (1746)
NheI (1903)
XmnI (1959)
AgeI (1989)
P15A origin
AgeI (2313)
ds-ori

FIG. 35PPP

pCALO-3:

```
     BglII                                                  AatII
     ~~~~~                                                  ~~~~~~
   1 GATCTCATAA CTTCGTATAA TGTATGCTAT ACGAAGTTAT GACGTCTAAT
     CTAGAGTATT GAAGCATATT ACATACGATA TGCTTCAATA CTGCAGATTA

  51 GTGAGTTAGC TCACTCATTA GGCACCCCAG GCTTTACACT TTATGCTTCC
     CACTCAATCG AGTGAGTAAT CCGTGGGGTC CGAAATGTGA AATACGAAGG

 101 GGCTCGTATG TTGTGTGGAA TTGTGAGCGG ATAACAATTT CACACAGGAA
     CCGAGCATAC AACACACCTT AACACTCGCC TATTGTTAAA GTGTGTCCTT

                                XbaI                    SphI
                               ~~~~~~~                  ~~~~~~
 151 ACAGCTATGA CCATGATTAC GAATTTCTAG ACCCCCCCCC CGCATGCCAT
     TGTCGATACT GGTACTAATG CTTAAAGATC TGGGGGGGGG GCGTACGGTA

                                          HindIII
                                          ~~~~~~
 201 AACTTCGTAT AATGTACGCT ATACGAAGTT ATAAGCTTGA CCTGTGAAGT
     TTGAAGCATA TTACATGCGA TATGCTTCAA TATTCGAACT GGACACTTCA
```

FIG. 35QQQ

PacI

```
                                                          ~~~~~~~~~
251  GAAAAATGGC GCAGATTGTG CGACATTTTT TTTGTCTGCC GTTTAATTAA
     CTTTTTACCG CGTCTAACAC GCTGTAAAAA AAACAGACGG CAAATTAATT

               FseI
            ~~~~~~~~~~
301  GGGGGGGGGC CGGCCATTAT CAAAAAGGAT CTCAAGAAGA TCCTTTGATC
     CCCCCCCCCG GCCGGTAATA GTTTTTCCTA GAGTTCTTCT AGGAAACTAG

351  TTTTCTACGG GGTCTGACGC TCAGTGGAAC GAAAACTCAC GTTAAGGGAT
     AAAAGATGCC CCAGACTGCG AGTCACCTTG CTTTTGAGTG CAATTCCCTA

401  TTTGGTCATG AGATTATCAA AAAGGATCTT CACCTAGATC CTTTTAAATT
     AAACCAGTAC TCTAATAGTT TTTCCTAGAA GTGGATCTAG GAAAATTTAA

451  AAAAATGAAG TTTTAAATCA ATCTAAAGTA TATATGAGTA AACTTGGTCT
     TTTTTACTTC AAAATTTAGT TAGATTTCAT ATATACTCAT TTGAACCAGA

501  GACAGTTACC CAATGCTTAA TCAGTGAGGC ACCTATCTCA GCGATCTGTC
     CTGTCAATGG GTTACGAATT AGTCACTCCG TGGATAGAGT CGCTAGACAG

551  TATTTCGTTC ATCCATAGTT GCCTGACTCC CCGTCGTGTA GATAACTACG
     ATAAAGCAAG TAGGTATCAA CGGACTGAGG GGCAGCACAT CTATTGATGC
```

FIG. 35RRR

```
601  ATACGGGAGG GCTTACCATC TGGCCCCAGT GCTGCAATGA TACCGCGAGA
     TATGCCCTCC CGAATGGTAG ACCGGGGTCA CGACGTTACT ATGGCGCTCT

651  CCCACGCTCA CCGGCTCCAG ATTTATCAGC AATAAACCAG CCAGCCGGAA
     GGGTGCGAGT GGCCGAGGTC TAAATAGTCG TTATTTGGTC GGTCGGCCTT

701  GGGCCGAGCG CAGAAGTGGT CCTGCAACTT TATCCGCCTC CATCCAGTCT
     CCCGGCTCGC GTCTTCACCA GGACGTTGAA ATAGGCGGAG GTAGGTCAGA

751  ATTAACTGTT GCCGGGAAGC TAGAGTAAGT AGTTCGCCAG TTAATAGTTT
     TAATTGACAA CGGCCCTTCG ATCTCATTCA TCAAGCGGTC AATTATCAAA

801  GCGCAACGTT GTTGCCATTG CTACAGGCAT CGTGGTGTCA CGCTCGTCGT
     CGCGTTGCAA CAACGGTAAC GATGTCCGTA GCACCACAGT GCGAGCAGCA

851  TTGGTATGGC TTCATTCAGC TCCGGTTCCC AACGATCAAG GCGAGTTACA
     AACCATACCG AAGTAAGTCG AGGCCAAGGG TTGCTAGTTC CGCTCAATGT

901  TGATCCCCCA TGTTGTGCAA AAAAGCGGTT AGCTCCTTCG GTCCTCCGAT
     ACTAGGGGGT ACAACACGTT TTTTCGCCAA TCGAGGAAGC CAGGAGGCTA

951  CGTTGTCAGA AGTAAGTTGG CCGCAGTGTT ATCACTCATG GTTATGGCAG
     GCAACAGTCT TCATTCAACC GGCGTCACAA TAGTGAGTAC CAATACCGTC
```

FIG. 35SSS

```
1001  CACTGCATAA TTCTCTTACT GTCATGCCAT CCGTAAGATG CTTTTCTGTG
      GTGACGTATT AAGAGAATGA CAGTACGGTA GGCATTCTAC GAAAAGACAC

1051  ACTGGTGAGT ACTCAACCAA GTCATTCTGA GAATAGTGTA TGCGGCGACC
      TGACCACTCA TGAGTTGGTT CAGTAAGACT CTTATCACAT ACGCCGCTGG

1101  GAGTTGCTCT TGCCCGGCGT CAATACGGGA TAATACCGCG CCACATAGCA
      CTCAACGAGA ACGGGCCGCA GTTATGCCCT ATTATGGCGC GGTGTATCGT

                                   XmnI
                                   ~~~~~~~~~~~

1151  GAACTTTAAA AGTGCTCATC ATTGGAAAAC GTTCTTCGGG GCGAAAACTC
      CTTGAAATTT TCACGAGTAG TAACCTTTTG CAAGAAGCCC CGCTTTTGAG

1201  TCAAGGATCT TACCGCTGTT GAGATCCAGT TCGATGTAAC CCACTCGCGC
      AGTTCCTAGA ATGGCGACAA CTCTAGGTCA AGCTACATTG GGTGAGCGCG

1251  ACCCAACTGA TCCTCAGCAT CTTTTACTTT CACCAGCGTT TCTGGGTGAG
      TGGGTTGACT AGGAGTCGTA GAAAATGAAA GTGGTCGCAA AGACCCACTC

1301  CAAAAACAGG AAGGCAAAAT GCCGCAAAAA AGGGAATAAG GGCGACACGG
      GTTTTTGTCC TTCCGTTTTA CGGCGTTTTT TCCCTTATTC CCGCTGTGCC

1351  AAATGTTGAA TACTCATACT CTTCCTTTTT CAATATTATT GAAGCATTTA
```

FIG. 35TTT

```
        TTTACAACTT ATGAGTATGA GAAGGAAAAA GTTATAATAA CTTCGTAAAT

                                                    BsrGI
                                                   ~~~~~~~
1401    TCAGGGTTAT TGTCTCATGA GCGGATACAT ATTTGAATGT ACATGAAATT
        AGTCCCAATA ACAGAGTACT CGCCTATGTA TAAACTTACA TGTACTTTAA

1451    GTAAACGTTA ATATTTTGTT AAAATTCGCG TTAAATTTTT GTTAAATCAG
        CATTTGCAAT TATAAAACAA TTTTAAGCGC AATTTAAAAA CAATTTAGTC

1501    CTCATTTTTT AACCAATAGG CCGAAATCGG CAAAATCCCT TATAAATCAA
        GAGTAAAAAA TTGGTTATCC GGCTTTAGCC GTTTTAGGGA ATATTTAGTT

1551    AAGAATAGAC CGAGATAGGG TTGAGTGTTG TTCCAGTTTG GAACAAGAGT
        TTCTTATCTG GCTCTATCCC AACTCACAAC AAGGTCAAAC CTTGTTCTCA

1601    CCACTATTAA AGAACGTGGA CTCCAACGTC AAAGGGCGAA AAACCGTCTA
        GGTGATAATT TCTTGCACCT GAGGTTGCAG TTTCCCGCTT TTTGGCAGAT

1651    TCAGGGCGAT GGCCCACTAC GAGAACCATC ACCCTAATCA AGTTTTTTGG
        AGTCCCGCTA CCGGGTGATG CTCTTGGTAG TGGGATTAGT TCAAAAAACC

                                                      BanII
                                                     ~~~~~~
```

FIG. 35UUU

```
1701  GGTCGAGGTG CCGTAAAGCA CTAAATCGGA ACCCTAAAGG GAGCCCCCGA
      CCAGCTCCAC GGCATTTCGT GATTTAGCCT TGGGATTTCC CTCGGGGGCT

1751  TTTAGAGCTT GACGGGGAAA GCCGGCGAAC GTGGCGAGAA AGGAAGGGAA
      AAATCTCGAA CTGCCCCTTT CGGCCGCTTG CACCGCTCTT TCCTTCCCTT

1801  GAAAGCGAAA GGAGCGGGCG CTAGGGCGCT GGCAAGTGTA GCGGTCACGC
      CTTTCGCTTT CCTCGCCCGC GATCCCGCGA CCGTTCACAT CGCCAGTGCG

1851  TGCGCGTAAC CACCACACCC GCCGCGCTTA ATGCGCCGCT ACAGGGCGCG
      ACGCGCATTG GTGGTGTGGG CGGCGCGAAT TACGCGGCGA TGTCCCGCGC

            NheI
          ~~~~~~~
1901  TGCTAGCGGA GTGTATACTG GCTTACTATG TTGGCACTGA TGAGGGTGTC
      ACGATCGCCT CACATATGAC CGAATGATAC AACCGTGACT ACTCCCACAG

            XmnI                                    AgeI
          ~~~~~~~~~~~                             ~~~~~~~
1951  AGTGAAGTGC TTCATGTGGC AGGAGAAAAA AGGCTGCACC GGTGCGTCAG
      TCACTTCACG AAGTACACCG TCCTCTTTTT TCCGACGTGG CCACGCAGTC

2001  CAGAATATGT GATACAGGAT ATATTCCGCT TCCTCGCTCA CTGACTCGCT
      GTCTTATACA CTATGTCCTA TATAAGGCGA AGGAGCGAGT GACTGAGCGA
```

FIG. 35VVV

```
2051  ACGCTCGGTC GTTCGACTGC GGCGAGCGGA AATGGCTTAC GAACGGGGCG
      TGCGAGCCAG CAAGCTGACG CCGCTCGCCT TTACCGAATG CTTGCCCCGC

2101  GAGATTTCCT GGAAGATGCC AGGAAGATAC TTAACAGGGA AGTGAGAGGG
      CTCTAAAGGA CCTTCTACGG TCCTTCTATG AATTGTCCCT TCACTCTCCC

2151  CCGCGGCAAA GCCGTTTTTC CATAGGCTCC GCCCCCCTGA CAAGCATCAC
      GGCGCCGTTT CGGCAAAAAG GTATCCGAGG CGGGGGGACT GTTCGTAGTG

2201  GAAATCTGAC GCTCAAATCA GTGGTGGCGA AACCCGACAG GACTATAAAG
      CTTTAGACTG CGAGTTTAGT CACCACCGCT TTGGGCTGTC CTGATATTTC

2251  ATACCAGGCG TTTCCCCCTG GCGGCTCCCT CCTGCGCTCT CCTGTTCCTG
      TATGGTCCGC AAAGGGGGAC CGCCGAGGGA GGACGCGAGA GGACAAGGAC

                    AgeI
                   ~~~~~~
2301  CCTTTCGGTT TACCGGTGTC ATTCCGCTGT TATGGCCGCG TTTGTCTCAT
      GGAAAGCCAA ATGGCCACAG TAAGGCGACA ATACCGGCGC AAACAGAGTA

2351  TCCACGCCTG ACACTCAGTT CCGGGTAGGC AGTTCGCTCC AAGCTGGACT
      AGGTGCGGAC TGTGAGTCAA GGCCCATCCG TCAAGCGAGG TTCGACCTGA
```

FIG. 35WWW

```
2401  GTATGCACGA ACCCCCCGTT CAGTCCGACC GCTGCGCCTT ATCCGGTAAC
      CATACGTGCT TGGGGGGCAA GTCAGGCTGG CGACGCGGAA TAGGCCATTG

2451  TATCGTCTTG AGTCCAACCC GGAAAGACAT GCAAAAGCAC CACTGGCAGC
      ATAGCAGAAC TCAGGTTGGG CCTTTCTGTA CGTTTTCGTG GTGACCGTCG

2501  AGCCACTGGT AATTGATTTA GAGGAGTTAG TCTTGAAGTC ATGCGCCGGT
      TCGGTGACCA TTAACTAAAT CTCCTCAATC AGAACTTCAG TACGCGGCCA

2551  TAAGGCTAAA CTGAAAGGAC AAGTTTTAGT GACTGCGCTC CTCCAAGCCA
      ATTCCGATTT GACTTTCCTG TTCAAAATCA CTGACGCGAG GAGGTTCGGT

2601  GTTACCTCGG TTCAAAGAGT TGGTAGCTCA GAGAACCTAC GAAAAACCGC
      CAATGGAGCC AAGTTTCTCA ACCATCGAGT CTCTTGGATG CTTTTTGGCG

2651  CCTGCAAGGC GGTTTTTTCG TTTTCAGAGC AAGAGATTAC GCGCAGACCA
      GGACGTTCCG CCAAAAAAGC AAAAGTCTCG TTCTCTAATG CGCGTCTGGT

                                  BglII

2701  AAACGATCTC AAGAAGATCA TCTTATTA
      TTTGCTAGAG TTCTTCTAGT AGAATAAT
```

FIG. 35XXX

M1: PCR using template

NoVspAatII: TAGACGTC

M2: synthesis

BloxA-A: TATGAGATCTCATAACTTCGTATAATGTACGCTATACG-
AAGTTAT

BloxA-B: TAATAACTTCGTATAGCATACATTATACGAAGTTATG-
AGATCTCA

M3: PCR, NoVspAatII as second oligo

XloxS-muta: CATTTTTTGCCCTCGTTATCTACGCATGCGATAACTTCGTA-
TAGCGTACATTATACGAAGTTATTCTAGACATGGTCATAGCTGTTTCCTG

M7-I: PCR

gIIINEW-fow: GGGGGGAATTCGGTGGTGGTGGATCTGCGTGCGCTG-
AAACGGTTGAAAGTTG

gIIINEW-rev: CCCCCCCAAGCTTATCAAGACTCCTTATTACG

M7-II: PCR

gIIIss-fow: GGGGGGGGAATTCGGAGGCGGTTCCGGTGGTGGC

M7-III: PCR

gIIIsupernew-fow: GGGGGGGGAATTCGAGCAGAAGCTGATCTCT-
GAGGAGGATCTGTAGGGTGGTGGCTCTGGTTCCGGTGATTTTG

FIG. 35YYY

M8: synthesis

lox514-A: CCATAACTTCGTATAATGTACGCTATACGAAGTTATA

lox514-B: AGCTTATAACTTCGTATAGCGTACATTATACGAAGT-TATGGCATG

M9II: synthesis

M9II-fow: AGCTTGACCTGTGAAGTGAAAAATGGCGCAGATT-GTGCGACATTTTTTTTGTCTGCCGTTTAATTAAAGGGGGGGT

M9II-rev: GTACACCCCCCCCCAGGCCGGCCCCCCCCCCCTTTAA-TTAAACGGCAGACAAAAAAAAATGTCGCACAATCTGCG

M10II: assembly PCR with template

bla-fow: GGGGGGGTGTACATTCAAATATGTATCCGCTCATG

bla-seq4: GGGTTACATCGAACTGGATCTC

bla1-muta: CCAGTTCGATGTAACCCACTCGCGCACCCAACTGATC-CTCAGCATCTTTTACTTTCACC

blaII-muta: ACTCTAGCTTCCCGGCAACAGTTAATAGACTGGATG-GAGGCGG

bla-NEW: CTGTTGCCGGGAAGCTAGAGTAAG

bla-rev: CCCCCCCTTAATTAAGGGGGGGGCCGGCCATTATCAAA-AAGGATCTCAAGAAGATCC

M11II/III: PCR, site-directed mutagenesis

FIG. 35ZZZ

f1-fow: GGGGGGGGCTAGCACGCGCCCTGTAGCGGCGCATTAA

f1-rev: CCCCCCCTGTACATGAAATTGTAAACGTTAATATTTTG

f1-t133.muta: GGGCGATGGCCCACTACGAGAACCATCACCCTAATC

M12: assembly PCR using template

p15-fow: GGGGGGAGATCTAATAAGATGATCTTCTTGAG

p15-NEWI: GAGTTGGTAGCTCAGAGAACCTACGAAAAACCGCCCTG-CAAGGCG

p15-NEWII: GTAGGTTCTCTGAGCTACCAACTC

p15-NEWIII: GTTTCCCCCTGGCGGCTCCCTCCTGCGCTCTCCTGTTCCT-GCC

p15-NEWIV: AGGAGGGAGCCGCCAGGGGGAAAC

p15-rev: GACATCAGCGCTAGCGGAGTGTATAC

M13: synthesis

BloxXB-A: GATCTCATAACTTCGTATAATGTATGCTATACGAAGTTA-TTCA

BloxXB-B: GATCTGAATAACTTCGTATAGCATACATTATACGAAGTTA-TGAGA

M14-Ext2: PCR, site-directed mutagenesis

ColEXT2-fow: GGGGGGGAGATCTGACCAAAATCCCTTAACGTGAG

Col-mutal: GGTATCTGCGCTCTGCTGTAGCCAGTTACCTTCGG

FIG. 35AAAA

Col-rev: CCCCCCCGCTAGCCATGTGAGCAAAAGGCCAGCAA

M17: assembly PCR using template

CAT-1: GGGACGTCGGGTGAGGTTCCAAC

CAT-2: CCATACGGAACTCCGGGTGAGCATTCATC

CAT-3: CCGGAGTTCCGTATGG

CAT-4: ACGTTTAAATCAAAACTGG

CAT-5: CCAGTTTTGATTTAAACGTAGCCAATATGGACAACTTCTTC-
GCCCCCGTTTTCACTATGGGCAAATATT

CAT-6: GGAAGATCTAGCACCAGGCGTTTAAG

M41: assembly PCR using template

LAC1: GAGGCCGGCCATCGAATGGCGCAAAAC

LAC2: CGCGTACCGTCCTCATGGGAGAAAATAATAC

LAC3: CCATGAGGACGGTACGCGACTGGGCGTGGAGCATCTGGTCGCA-
TTGGGTCACCAGCAAATCCGCTGTTAGCTGGCCCATTAAG

LAC4: GTCAGCGGCGGGATATAACATGAGCTGTCCTCGGTATCGTCG

LAC5: GTTATATCCCGCCGCTGACCACCATCAAAC

LAC6: CATCAGTGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGT4TTG-
GGAGCCAGGGTGGTTTTTC

LAC7: GGTTAATTAACCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCC-
AGCTGCATCAGTGAATCGGCCAAC

M41-MCS-fow: CTAGACTAGTGTTTAAACCGGACCGGGGGGGGGCTT-
AAGGGGGGGGGGGG

FIG. 35BBBB

M41-MCS-rev: CTAGCCCCCCCCCCCCTTAAGCCCCCCCCCGGTCCGGT-TTAAACACTAGT

M41-fow: CTAGACTAGTGTTTAAACCGGACCGGGGGGGGGGCTTAA-GGGGGGGGGGGG

M41-rev: CCCCCCCTTAAGTGGGCTGCAAAACAAAACGGCCTCC-TGTCAGGAAGCCGCTTTTATCGGGTAGCCTCACTGCCCGCTTTCC

M41-A2: GTTGTTGTGCCACGCGGTTAGGAATGTAATTCAGCTCCGC

M41-B1: AACCGCGTGGCACAACAAC

M41-B2: CTTCGTTCTACCATCGACACGACCACGCTGGCACCCAGTTG

M41-C1: GTGTCGATGGTAGAACGAAG

M41-CII: CCACAGCAATAGCATCCTGGTCATCCAGCGGATAGTT-AATAATCAGCCCACTGACACGTTGCGCGAG

M41-DI: GACCAGGATGCTATTGCTGTGG

M41-DII: CAGCGCGATTTGCTGGTGGCCCAATGCGACCAGATGC

M41-EI: CACCAGCAAATCGCGCTG

M41-EII: CCCGGACTCGGTAATGGCACGCATTGCGCCCAGCGCC

M41-FI: GCCATTACCGAGTCCGGG

<u>M42: synthesis</u>

Eco-H5-Hind-fow: AATTCCACCATCATCACCATTGACGTCTA

Eco-H5-Hind-rev: AGCTTAGACGTCAATGGTGATGATGGTGG

FIG. 35CCCC

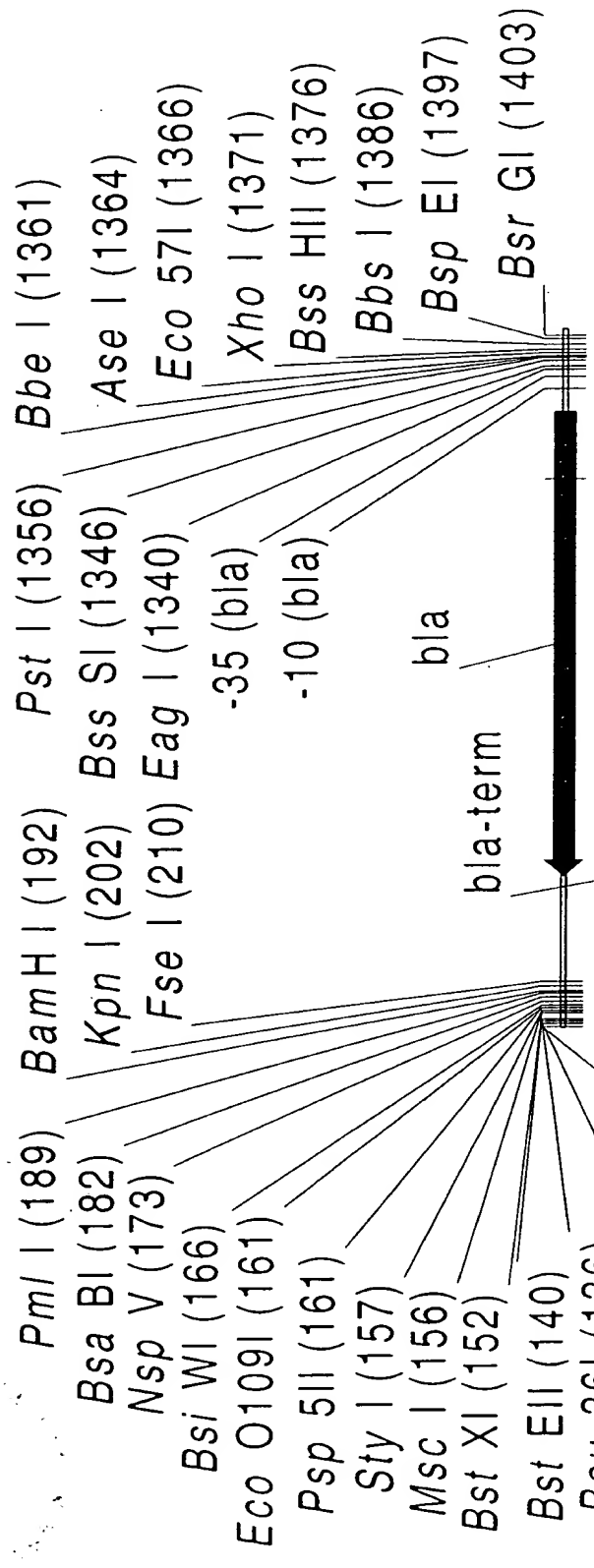

Pml I (189)
BamH I (192)
Pst I (1356)
Bbe I (1361)
Bsa BI (182)
Kpn I (202)
Bss SI (1346)
Ase I (1364)
Nsp V (173)
Fse I (210)
Eag I (1340)
Eco 57I (1366)
Bsi WI (166)
-35 (bla)
Xho I (1371)
Eco O109I (161)
-10 (bla)
Bss HII (1376)
Psp 5II (161)
bla
Bbs I (1386)
Sty I (157)
Bsp EI (1397)
Msc I (156)
bla-term
Bsr GI (1403)
Bst XI (152)
Bst EII (140)
bla MCS
Bsu 36I (136)
1289 bp
Hpa I (132)
Mlu I (126)

FIG. 36A

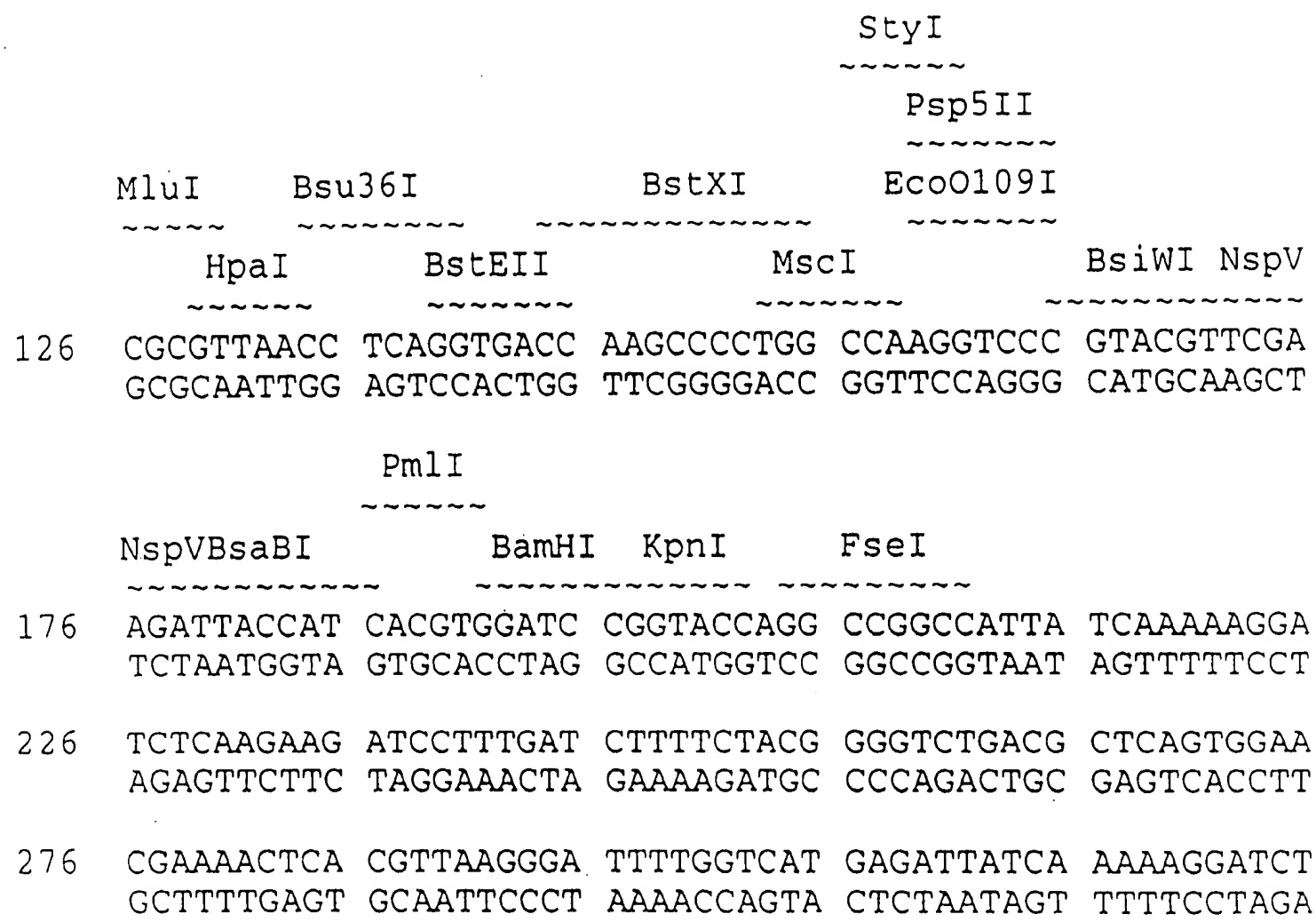

StyI
Psp5II
MluI
Bsu36I
BstXI
Eco0109I
HpaI
BstEII
MscI
BsiWI
NspV
PmlI
NspVBsaBI
BamHI
KpnI
FseI
126 CGCGTTAACC TCAGGTGACC AAGCCCCTGG CCAAGGTCCC GTACGTTCGA
GCGCAATTGG AGTCCACTGG TTCGGGGACC GGTTCCAGGG CATGCAAGCT
176 AGATTACCAT CACGTGGATC CGGTACCAGG CCGGCCATTA TCAAAAAGGA
TCTAATGGTA GTGCACCTAG GCCATGGTCC GGCCGGTAAT AGTTTTTCCT
226 TCTCAAGAAG ATCCTTTGAT CTTTTCTACG GGGTCTGACG CTCAGTGGAA
AGAGTTCTTC TAGGAAACTA GAAAAGATGC CCCAGACTGC GAGTCACCTT
276 CGAAAACTCA CGTTAAGGGA TTTTGGTCAT GAGATTATCA AAAAGGATCT
GCTTTTGAGT GCAATTCCCT AAAACCAGTA CTCTAATAGT TTTTCCTAGA

FIG. 36B

```
326  TCACCTAGAT CCTTTTAAAT TAAAAATGAA GTTTTAAATC AATCTAAAGT
     AGTGGATCTA GGAAAATTTA ATTTTTACTT CAAAATTTAG TTAGATTTCA

376  ATATATGAGT AAACTTGGTC TGACAGTTAC CAATGCTTAA TCAGTGAGGC
     TATATACTCA TTTGAACCAG ACTGTCAATG GTTACGAATT AGTCACTCCG

426  ACCTATCTCA GCGATCTGTC TATTTCGTTC ATCCATAGTT GCCTGACTCC
     TGGATAGAGT CGCTAGACAG ATAAAGCAAG TAGGTATCAA CGGACTGAGG

476  CCGTCGTGTA GATAACTACG ATACGGGAGG GCTTACCATC TGGCCCCAGT
     GGCAGCACAT CTATTGATGC TATGCCCTCC CGAATGGTAG ACCGGGGTCA

526  GCTGCAATGA TACCGCGAGA CCCACGCTCA CCGGCTCCAG ATTTATCAGC
     CGACGTTACT ATGGCGCTCT GGGTGCGAGT GGCCGAGGTC TAAATAGTCG

576  AATAAACCAG CCAGCCGGAA GGGCCGAGCG CAGAAGTGGT CCTGCAACTT
     TTATTTGGTC GGTCGGCCTT CCCGGCTCGC GTCTTCACCA GGACGTTGAA

626  TATCCGCCTC CATCCAGTCT ATTAACTGTT GCCGGGAAGC TAGAGTAAGT
     ATAGGCGGAG GTAGGTCAGA TAATTGACAA CGGCCCTTCG ATCTCATTCA

676  AGTTCGCCAG TTAATAGTTT GCGCAACGTT GTTGCCATTG CTACAGGCAT
     TCAAGCGGTC AATTATCAAA CGCGTTGCAA CAACGGTAAC GATGTCCGTA
```

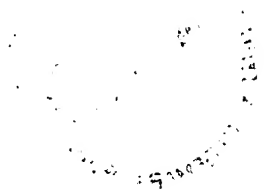
FIG. 36C

```
 726  CGTGGTGTCA CGCTCGTCGT TTGGTATGGC TTCATTCAGC TCCGGTTCCC
      GCACCACAGT GCGAGCAGCA AACCATACCG AAGTAAGTCG AGGCCAAGGG

 776  AACGATCAAG GCGAGTTACA TGATCCCCCA TGTTGTGCAA AAAAGCGGTT
      TTGCTAGTTC CGCTCAATGT ACTAGGGGGT ACAACACGTT TTTTCGCCAA

 826  AGCTCCTTCG GTCCTCCGAT CGTTGTCAGA AGTAAGTTGG CCGCAGTGTT
      TCGAGGAAGC CAGGAGGCTA GCAACAGTCT TCATTCAACC GGCGTCACAA

 876  ATCACTCATG GTTATGGCAG CACTGCATAA TTCTCTTACT GTCATGCCAT
      TAGTGAGTAC CAATACCGTC GTGACGTATT AAGAGAATGA CAGTACGGTA

 926  CCGTAAGATG CTTTTCTGTG ACTGGTGAGT ACTCAACCAA GTCATTCTGA
      GGCATTCTAC GAAAAGACAC TGACCACTCA TGAGTTGGTT CAGTAAGACT

 976  GAATAGTGTA TGCGGCGACC GAGTTGCTCT TGCCCGGCGT CAATACGGGA
      CTTATCACAT ACGCCGCTGG CTCAACGAGA ACGGGCCGCA GTTATGCCCT

1026  TAATACCGCG CCACATAGCA GAACTTTAAA AGTGCTCATC ATTGGAAAAC
      ATTATGGCGC GGTGTATCGT CTTGAAATTT TCACGAGTAG TAACCTTTTG

1076  GTTCTTCGGG GCGAAAACTC TCAAGGATCT TACCGCTGTT GAGATCCAGT
      CAAGAAGCCC CGCTTTTGAG AGTTCCTAGA ATGGCGACAA CTCTAGGTCA
```

FIG. 36D

```
1126  TCGATGTAAC CCACTCGTGC ACCCAACTGA TCTTCAGCAT CTTTTACTTT
      AGCTACATTG GGTGAGCACG TGGGTTGACT AGAAGTCGTA GAAAATGAAA
                     BssSI                Eco57I
                    ~~~~~~               ~~~~~~

1176  CACCAGCGTT TCTGGGTGAG CAAAAACAGG AAGGCAAAAT GCCGCAAAAA
      GTGGTCGCAA AGACCCACTC GTTTTTGTCC TTCCGTTTTA CGGCGTTTTT

1226  AGGGAATAAG GGCGACACGG AAATGTTGAA TACTCATACT CTTCCTTTTT
      TCCCTTATTC CCGCTGTGCC TTTACAACTT ATGAGTATGA GAAGGAAAAA

1276  CAATATTATT GAAGCATTTA TCAGGGTTAT TGTCTCATGA GCGGATACAT
      GTTATAATAA CTTCGTAAAT AGTCCCAATA ACAGAGTACT CGCCTATGTA

                                 PstI                  XhoI
                                ~~~~~~~               ~~~~~~
                      EagI    BssSI        BbeI  AseI     BssHII
                     ~~~~~~~~~~~~~      ~~~~~~~~~~~~~       ~
1326  ATTTGAATGT ACTCGGCCGC ACGAGCTGCA GGCGCCATTA ATGGCTCGAG
      TAAACTTACA TGAGCCGGCG TGCTCGACGT CCGCGGTAAT TACCGAGCTC

      BssHII                  BspEI BsrGI
      ~~~~~                  ~~~~~~~~~~~~
```

FIG. 36E



```
1376  CGCGCTTCAG CGCTTTGTCT TCCGGATGTA CATGAAATT
      GCGCGAAGTC GCGAAACAGA AGGCCTACAT GTACTTTAA
          Eco57I         BbsI
          ~~~~~~         ~~~~~~~
```

FIG. 36F

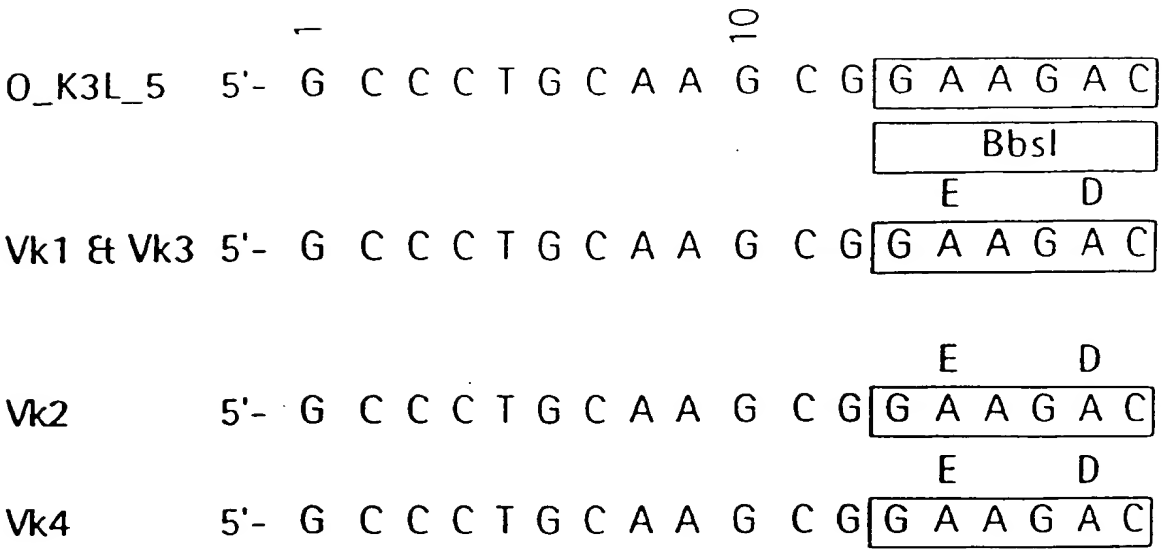

1
10
O_K3L_5 5'- G C C C T G C A A G C G G A A G A C
BbsI
E D
Vk1 & Vk3 5'- G C C C T G C A A G C G G A A G A C
E D
Vk2 5'- G C C C T G C A A G C G G A A G A C
E D
Vk4 5'- G C C C T G C A A G C G G A A G A C

FIG. 37A

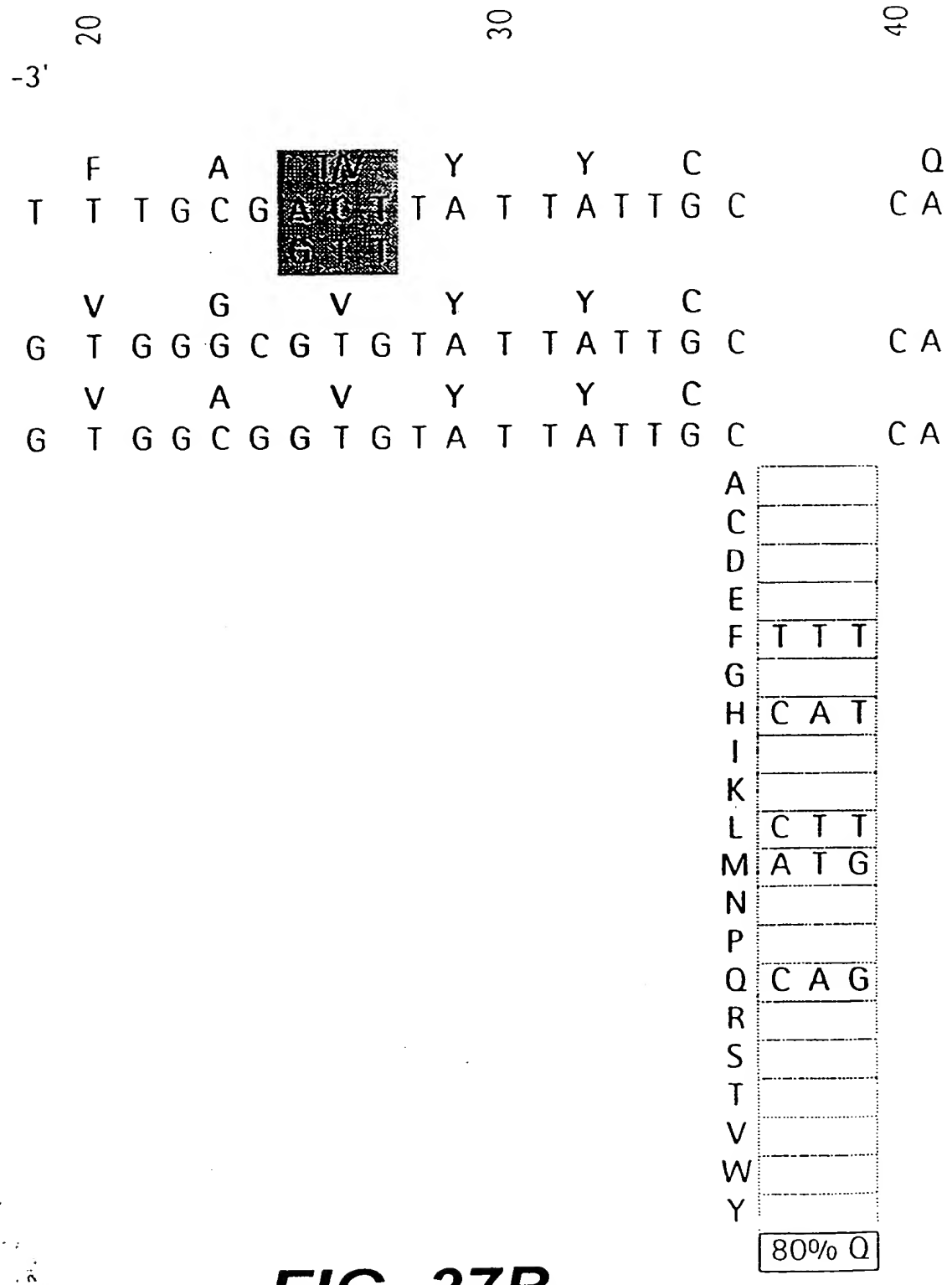

20
30
40
-3'
F A T/V Y Y C Q
T T T G C G A/C/T T A T T A T T G C C A
V G V Y Y C
G T G G G C G T G T A T T A T T G C C A
V A V Y Y C
G T G G C G G T G T A T T A T T G C C A
A
C
D
E
F T T T
G
H C A T
I
K
L C T T
M A T G
N
P
Q C A G
R
S
T
V
W
Y
80% Q

FIG. 37B

50 60

3'- G G A

T
G A C C T

T
G A C C T

T
G A C C T

G C T			G C T		G C T
G A T	G A T	G A T	G A T		G A T
G A G			G A G		G A G
T T T			T T T		T T T
G G T	G G T	G G T	G G T		G G T
C A T			C A T		C A T
A T T			A T T		A T T
A A G			A A G		A A G
C T T			C T T		C T T
A T G			A T G		A T G
A A T	A A T	A A T	A A T		A A T
			C C T	C C T	C C T
C A G			C A G		C A G
C G T			C G T		C G T
T C T	T C T	T C T	T C T	T C T	T C T
A C T			A C T		A C T
G T T			G T T		G T T
T G G			T G G		T G G
T A T	T A T		T A T		T A T
50% Y				80% P	

FIG. 37C

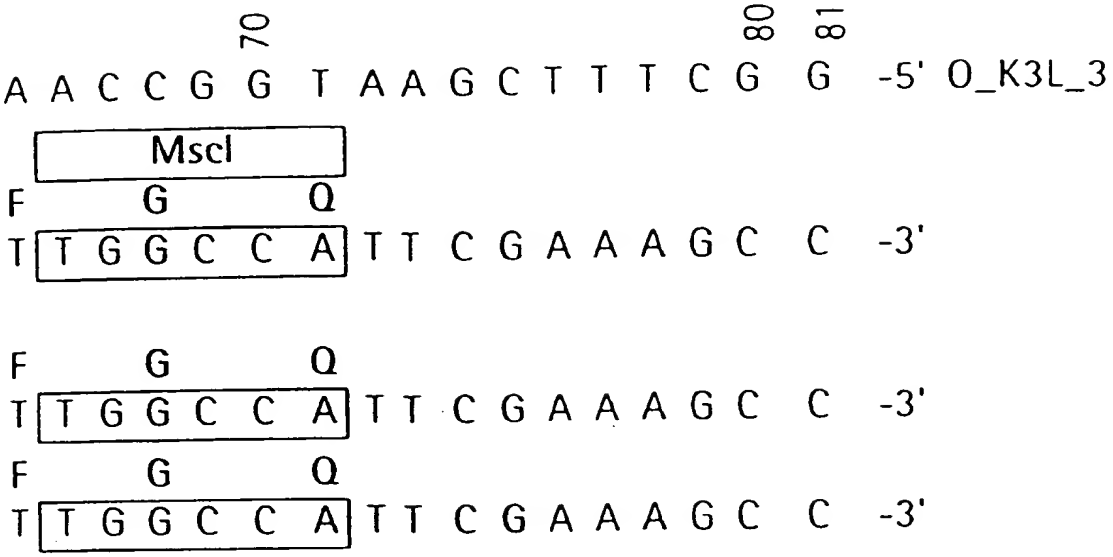

70
80
81
A A C C G G T A A G C T T T C G G -5' O_K3L_3
MscI
F G Q
T T G G C C A T T C G A A A G C C -3'
F G Q
T T G G C C A T T C G A A A G C C -3'
F G Q
T T G G C C A T T C G A A A G C C -3'

FIG. 37D

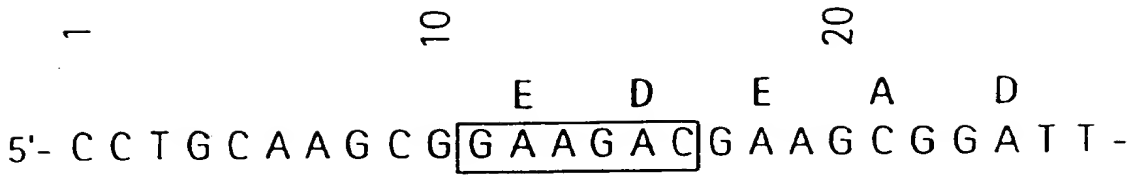


FIG. 38A

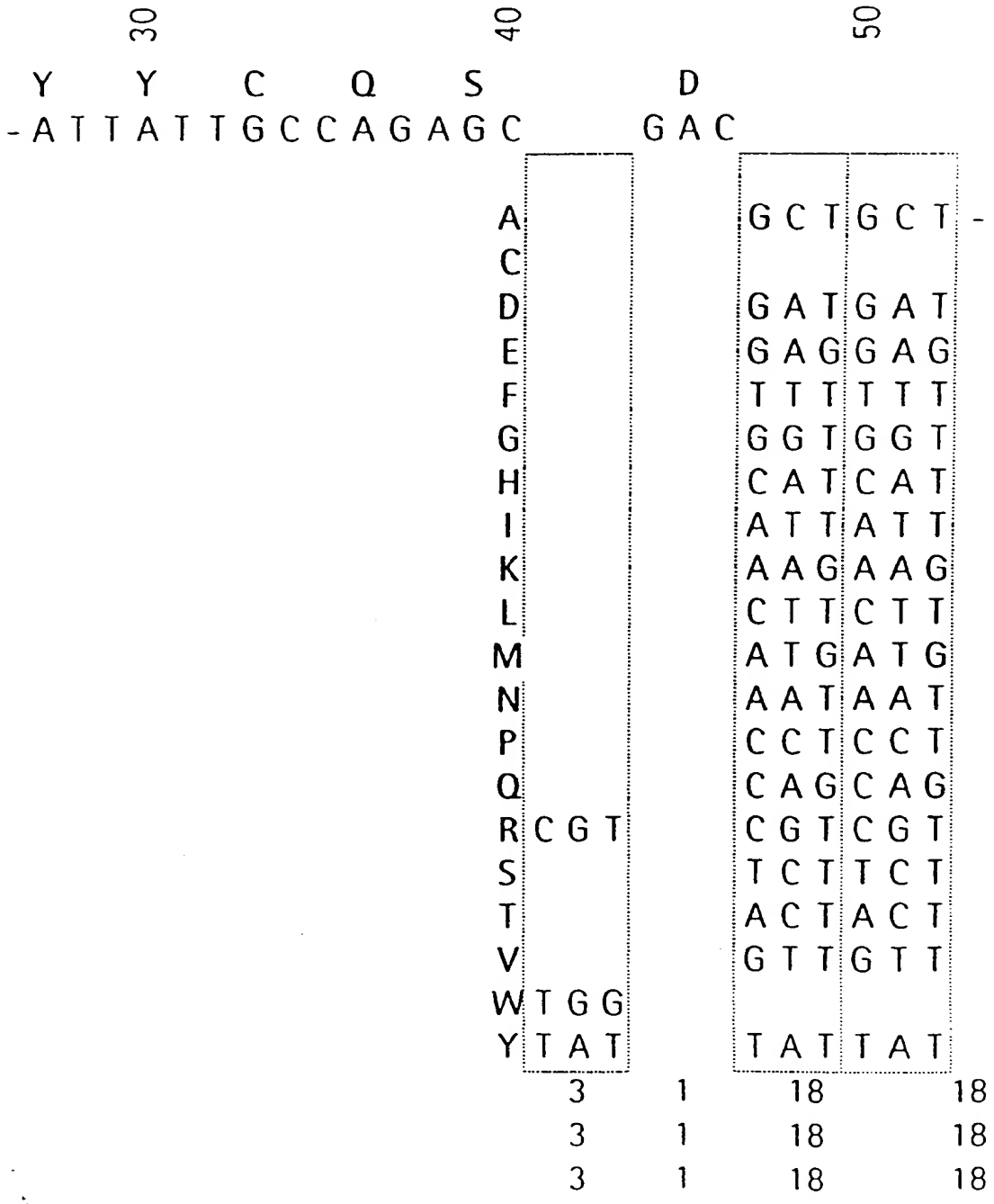

30
40
50
Y Y C Q S D
-A T T A T T G C C A G A G C G A C
A G C T G C T -
C
D G A T G A T
E G A G G A G
F T T T T T T
G G G T G G T
H C A T C A T
I A T T A T T
K A A G A A G
L C T T C T T
M A T G A T G
N A A T A A T
P C C T C C T
Q C A G C A G
R C G T C G T C G T
S T C T T C T
T A C T A C T
V G T T G T T
W T G G
Y T A T T A T T A T
3 1 18 18
3 1 18 18
3 1 18 18

FIG. 38B

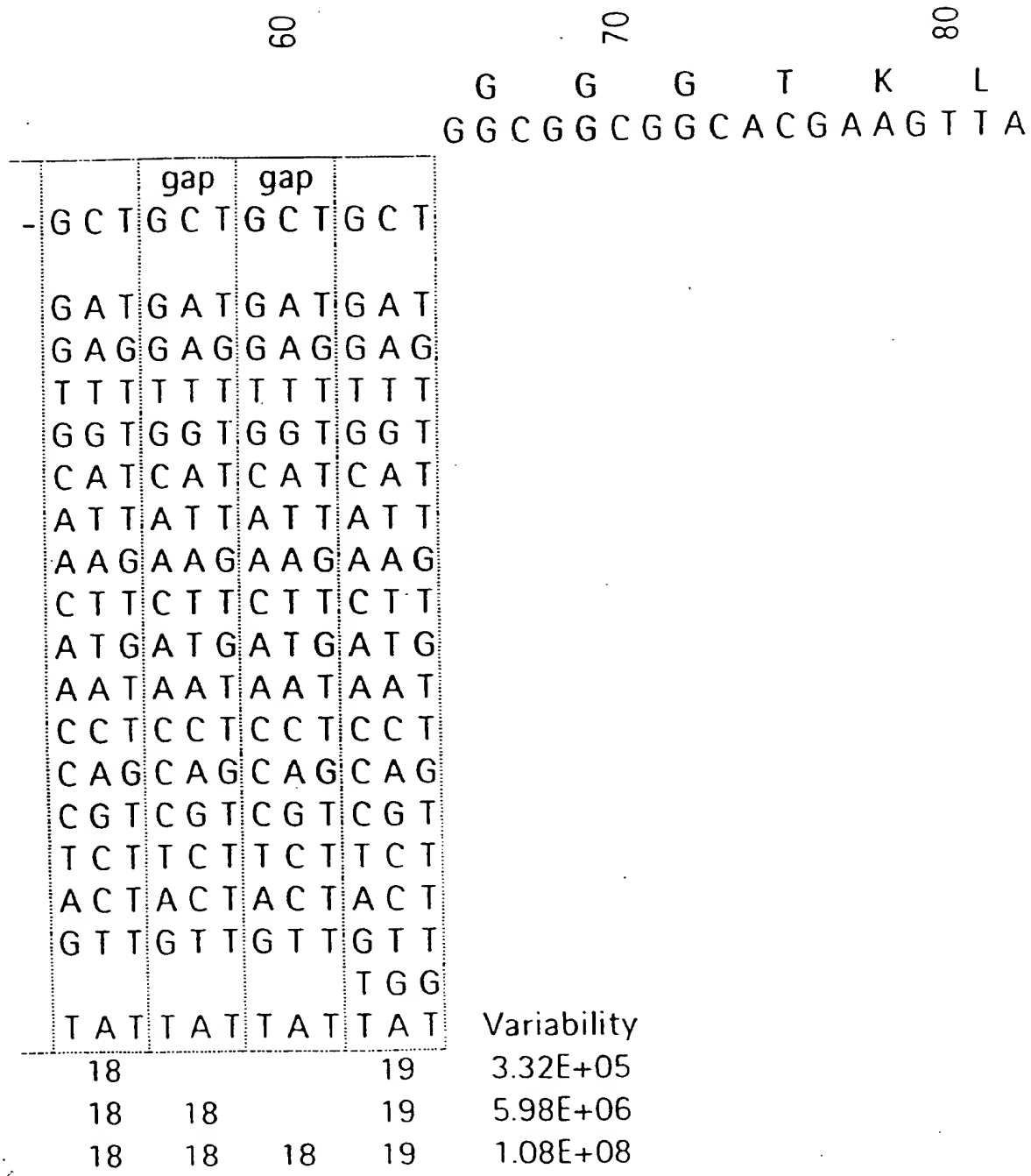

60
70
80
G G G T K L
G G C G G C G G C A C G A A G T T A
gap gap
- G C T G C T G C T G C T
G A T G A T G A T G A T
G A G G A G G A G G A G
T T T T T T T T T T T T
G G T G G T G G T G G T
C A T C A T C A T C A T
A T T A T T A T T A T T
A A G A A G A A G A A G
C T T C T T C T T C T T
A T G A T G A T G A T G
A A T A A T A A T A A T
C C T C C T C C T C C T
C A G C A G C A G C A G
C G T C G T C G T C G T
T C T T C T T C T T C T
A C T A C T A C T A C T
G T T G T T G T T G T T
T G G
T A T T A T T A T T A T
Variability
18 19 3.32E+06
18 18 19 5.98E+06
18 18 18 19 1.08E+08

FIG. 38C

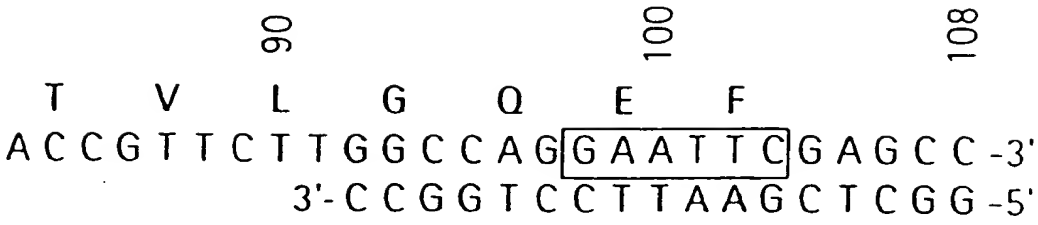

90
100
108
T V L G Q E F
ACCGTTCTTGGCCAGGAATTCGAGCC-3'
3'-CCGGTCCTTAAGCTCGG-5'

FIG. 38D

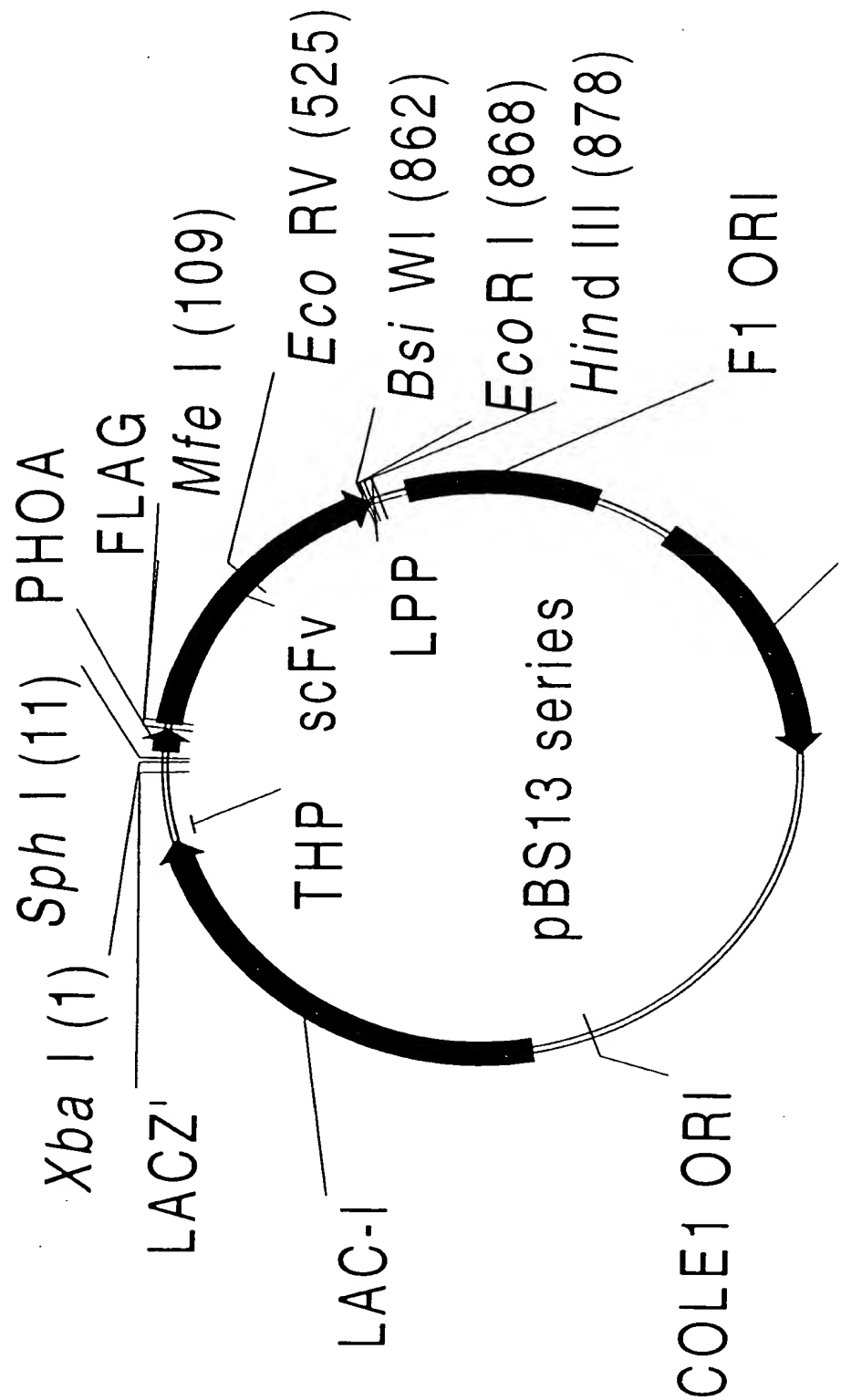

Xba I (1)
Sph I (11)
PHOA
FLAG
Mfe I (109)
Eco RV (525)
Bsi WI (862)
EcoR I (868)
Hind III (878)
F1 ORI
CM(R)
LACZ'
THP
scFv
LPP
pBS13 series
LAC-I
COLE1 ORI

FIG. 39

% soluble	κ1	κ2	κ3	κ4	λ1	λ2	λ3
H1A	61%	58%	52%	42%	90%	61%	60%
H1B	39%	48%	66%	48%	47%	39%	36%
H2	47%	57%	46%	49%	37%	36%	45%
H3	85%	67%	76%	61%	80%	71%	83%
H4	69%	52%	51%	44%	45%	33%	42%
H5	49%	49%	46%	67%	54%	46%	47%
H6	90%	58%	54%	47%	45%	50%	51%

Total amount compared to H3κ2	κ1	κ2	κ3	κ4	λ1	λ2	λ3
H1A	289%	94%	166%	272%	20%	150%	78%
H1B	219%	122%	89%	139%	117%	158%	101%
H2	186%	223%	208%	182%	126%	60%	97%
H3	50%		71%	54%	59%	130%	47%
H4	37%	55%	60%	77%	195%	107%	251%
H5	98%	201%	167%	83%	93%	128%	115%
H6	65%	117%	89%	109%	299%	215%	278%

FIG. 40A

Soluble amount compared to H3κ2	κ1	κ2	κ3	κ4	λ1	λ2	λ3
H1A	191%	88%	121%	122%	26%	211%	76%
H1B	124%	95%	83%	107%	79%	142%	59%
H2	126%	204%	139%	130%	66%	50%	70%
H3	63%	-	81%	49%	69%	143%	61%
H4	40%	47%	49%	54%	95%	55%	125%
H5	69%	158%	116%	80%	72%	84%	84%
H6	85%	122%	87%	77%	162%	162%	212%

	McPC
soluble	38%
%H3k2 total	117%
%H3k2 soluble	69%

FIG. 40B